

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 20:16:55 ; Search time 1457.41 Seconds
(without alignments)
11926.532 Million cell updates/sec

Title: US-10-764-316-7

Perfect score: 2493

Sequence: 1 ccggcgccggcgccggcgag.....aataaaccttttaaacctcc 2493

Scoring table:

OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 524920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_8.*

1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2493	100.0	2493	6	ABA02398
2	502	20.1	2279	14	AEB54684
3	495	19.9	2361	3	AAF18262
4	484	19.4	2336	12	ADE77038
5	431	17.3	2962	8	ABX62981
6	431	17.3	2962	13	ADI161704
7	431	17.3	2962	14	AEA43869
8	429	17.2	531	12	ADP66225
9	329	13.2	2492	6	ABL68660
10	329	13.2	2492	6	ABK84553
11	329	13.2	2492	8	ACA64921
12	329	13.2	2492	15	AEF92617
13	283	11.4	1932	6	ABA93631
14	283	11.4	1932	10	ADD18651
15	283	11.4	1932	12	ADP12821
16	283	11.4	1932	13	ADP14394
17	283	11.4	1932	13	ADP22911
18	283	11.4	1932	14	ADV42954

19	283	11.4	1932	14	ADX06581	Adx06581 Cyclin-de
20	259	10.4	1001	13	ADQ80920	Adq80920 Human phe
21	187	7.5	445	13	ADU13608	Adu13608 Solid tum
22	154	6.2	1001	13	ADQ80919	Adq80919 Human phe
23	120	4.8	968	11	ADI31786	Adi31786 Human cDN
24	120	4.8	968	13	ADS83853	Ads83853 Human lym
25	120	4.8	968	15	AEF92618	Aef92618 Human hea
26	102	4.1	1280	14	ADV97672	Adv97672 Human hea
27	100	4.0	286	2	AAV21143	Aav21143 Human hsp
28	100	4.0	469	2	AAV56356	Aav56356 Human hea
29	100	4.0	469	12	ADL32452	Adl32452 Human hea
30	100	4.0	469	14	AEB68778	Aeb68778 Human min
31	100	4.0	550	4	AAS01683	Aas01683 Human hea
32	100	4.0	592	8	ACA61270	Aca61270 Human hea
33	100	4.0	592	9	ACF35886	Acf35886 Human hea
34	100	4.0	714	8	ACC43397	Acc43397 5' UTR of
35	91	3.7	445	13	ADU13658	Adu13658 Solid tum
36	85	3.4	159	3	AAC09982	Aac09982 Human sec
37	76	3.0	475	9	ACH44271	Ach44271 Human foe
38	75	3.0	376	14	ACL54045	Ac154045 Human col
39	71	2.8	2386	2	AAT38809	Aat38809 Marmoset
40	60	2.4	60	6	ABN38808	Abn38808 Human spl
41	58	2.3	119	3	AAA94741	Aaa94741 Human HSP
42	50	2.0	50	6	ABZ02264	Abz02264 Human leu
43	50	2.0	50	12	ADP12652	Adp12652 50-mer ol
44	48	1.9	768	6	ABQ34182	Abq34182 Oligonuc
45	48	1.9	768	6	ABQ34183	Abq34183 Oligonuc

ALIGNMENTS

RESULT 1

ABA02398 standard; DNA; 2493 BP.

AC ABA02398;

DT 26-FEB-2002 (first entry)

DE Human heat shock protein HSPA7-encoding DNA.

KW Human; heat shock protein; HSPA7; SCZ gene; chromosome 1q22;
KW schizophrenia; schizoaffective disorder; susceptibility; diagnosis;
KW polymorphic marker; linkage disequilibrium; APOA2; FCER1G; FCGR2A;
KW D1S2675; B22624T; neuroleptic; gene therapy; drug screening;
KW in utero screening; ds.

OS Homo sapiens.

PN WO200180718-A2.

PD 01-NOV-2001.

PF 23-APR-2001; 2001WO-US013073.

PR 21-APR-2000; 2000US-0199114P.

PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.

PI Brzustowicz LM, Bassett AS;

DR WPI; 2002-049235/06.

PT Diagnosing susceptibility to schizophrenia in a patient, involves
PT detecting polymorphic marker allele within chromosome segment 1q22
PT bordered by D1S2705 and D1S1679 and linked to variant form of SCZ DNA
PT segment.

PS Claim 19; Page 64-66; 77pp; English.

CC This sequence represents DNA encoding the human heat shock protein HSPA7.
CC The HSPA7 gene is located on chromosome 1q22, a region thought to be

associated with schizophrenia and the closely related schizoaffective disorder. The invention identifies the HSPA7 gene as an SCZ gene, a variant form of which is associated with a schizophrenia phenotype. The invention relates to a novel method of diagnosing a patient's susceptibility to schizophrenia. The method involves determining the presence of an allele of a polymorphic marker linked to a variant form of an SCZ gene within a segment of chromosome 1q22 bordered by DIS2705 and DIS1679. The polymorphic marker allele is in phase with the variant form of SCZ, and its presence indicates a susceptibility to schizophrenia and related disorders. The polymorphic marker is APOA2, FGRIG, FGR2A, DIS2675, or preferably B428K24r. The invention also relates to a method for determining an alteration in an SCZ promoter sequence, where the alteration is associated with a schizophrenic condition, and a method for assessing a test compound for its ability to modulate the activity of an SCZ protein. The methods of the invention are useful for diagnosing schizophrenia or schizoaffective disorder, or a susceptibility to these conditions in a patient using a saliva, blood or buccal mucosal cell sample. The HSPA7 proteins and nucleotides have neuroleptic activity and may be used in gene therapy, and HSPA7 protein modulating compounds may be useful in the treatment of schizophrenia and related disorders. The invention also provides a highly accurate assay for in utero screening of fetuses for the presence of a variant SCZ allele, which will enable the administration of appropriate treatment at an early stage

Sequence 2493 BP; 554 A; 676 C; 794 G; 469 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2493;	DB 6;	Length 2493;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2493; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0
Qy	1	CCCCGGCGGGCGGGGAGGTCTTCGACTCGGGCGGGAAGGTTCGGGAAGGTTTCGCGGG	60	
Db	1			
Qy	61	GCGGGTTCGGGAGGTGCAAAAGATGAAAAACCCCGTGGAACGGAGCTTGACGATCCG	120	
Db	61	GCGGGTTCGGGAGGTGCAAAAGATGAAAAACCCCGTGGAACGGAGCTTGACGATCCG	120	
Qy	121	AGCCGGGTCGGCGGAGAGAACCAGCGGAGAGCCTCACTGCTAGGCCCCCTCGACGG	180	
Db	121	AGCCGGGTCGGCGGAGAGAAACCGAGGGAGAGCCTCACTGCTAGGCCCCCTCGACGG	180	
Qy	181	CGGAGCGGAGCAGCCTTCGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATGCAGCG	240	
Db	181	CGGAGCGGAGCAGCCTTCGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATGCAGCG	240	
Qy	241	CCCACGGGAGCTCGGGGTGGGATCGACTCTGGGCAACCACTACTCTGTGGTGGGCGTGT	300	
Db	241	CCCACGGGAGCTCGGGGTGGGATCGACTCTGGGCAACCACTACTCTGTGGTGGGCGTGT	300	
Qy	301	TCAGCAGGCGCGGTGGAGATCTCGGCCAACACCAAGGGCAACCGCACACCGCCCAAGCTA	360	
Db	301	TCAGCAGGCGCGGTGGAGATCTCGGCCAACACCAAGGGCAACCGCACACCGCCCAAGCTA	360	
Qy	361	CGTGCCCTTACCGACACCGAGCGGCTGTTCGGGACCGGGCCAGAGCAGCGCGCCCT	420	
Db	361	CGTGCCCTTACCGACACCGAGCGGCTGTTCGGGACCGGGCCAGAGCAGCGCGCCCT	420	
Qy	421	GAAACCCCAACACCGTCTTCGATGCCAAAGCGGCTGATCGGGCGCAAGTTTCGCGGACAC	480	
Db	421	GNAACCCCAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGCGGACAC	480	
Qy	481	CACGTTGCAGTCGGACATGAAGACATGCGCCCTTCCAGTGTGTTAGCGAGGGCGGCAAGCC	540	
Db	481	CACGTTGCAGTCGGACATGAAGACATGCGCCCTTCCAGTGTGTTAGCGAGGGCGGCAAGCC	540	
Qy	541	CAAAGTGGCGGTATGCTACCGGGGAGGACAGAAGCTTCTACCCCGAGAGATCTCTGTC	600	
Db	541	CAAAGTGGCGGTATGCTACCGGGGAGGACAGAAGCTTCTACCCCGAGAGATCTCTGTC	600	
Qy	601	CATGTTGTGACAAAGATGAAGAGACGCGCCGAGCGCTACCTGGGCGAGCCCGGTGAAGCA	660	
Db	601	CATGTTGTGACAAAGATGAAGAGACGCGCCGAGCGCTACCTGGGCGAGCCCGGTGAAGCA	660	

Qy	1741	TCACCAATGACAAGGGCCGGCTGAGCAAGAGGAGGAGATGTTTCATGAAGCCG	1800
Db	1741	TCACCAATGACAAGGGCCGGCTGAGCAAGAGGAGGAGTGGAGAGATGTTTCATGAAGCCG	1800
Qy	1801	AGCAGTACGGGGCTGAGGATCAGGCCCCAGAGGGACAGATGGCTGCCAAAACTCGCTGG	1860
Db	1801	AGCAGTACGGGGCTGAGGATCAGGCCCCAGAGGGACAGATGGCTGCCAAAACTCGCTGG	1860
Qy	1861	AGGCCCATGTCTTCCATGTGAAAGGTTCTTTTGCAGAGGAAAGCCTTTAGGGACAAGATTC	1920
Db	1861	AGGCCCATGTCTTCCATGTGAAAGGTTCTTTTGCAGAGGAAAGCCTTTAGGGACAAGATTC	1920
Qy	1921	CCGAAGAGGACAGCGCGCAAGTGCAGACAAAGTGTCAAGAGTCCTTGCTTGGCTGGAGC	1980
Db	1921	CCGAAGAGGACAGCGCGCAAGTGCAGACAAAGTGTCAAGAGTCCTTGCTTGGCTGGAGC	1980
Qy	1981	ACAACCACTGGCAGAGAGGAGAGTATGAGCATCAGAAGAGGAGCTGGAGCAAACTC	2040
Db	1981	ACAACCACTGGCAGAGAGGAGAGTATGAGCATCAGAAGAGGAGCTGGAGCAAACTC	2040
Qy	2041	GTGCCCCCATCTTCTCCAGGCTCTATGGGGGGCCTGTGTCCCTGGGGGGCAGCAGTTGTA	2100
Db	2041	GTGCCCCCATCTTCTCCAGGCTCTATGGGGGGCCTGTGTCCCTGGGGGGCAGCAGTTGTA	2100
Qy	2101	CGCTCAAGCCCAACAGGGGGAACCCAGCAGCCCGCCCATCATTTGAGAGGTTGATTGAA	2160
Db	2101	CGCTCAAGCCCAACAGGGGGAACCCAGCAGCCCGCCCATCATTTGAGAGGTTGATTGAA	2160
Qy	2161	TGGCCCTTCGTGATAAGTCAAGTGTGACTGTGAGGGCTATGCTATGGGCCCTTCTAGACTG	2220
Db	2161	TGGCCCTTCGTGATAAGTCAAGTGTGACTGTGAGGGCTATGCTATGGGCCCTTCTAGACTG	2220
Qy	2221	TCCTTCTATGATCTTGCCCTTCAGAGATGAAGGGCTTGGGGGGCTCTTCCCTCCAAAGCTA	2280
Db	2221	TCCTTCTATGATCTTGCCCTTCAGAGATGAAGGGCTTGGGGGGCTCTTCCCTCCAAAGCTA	2280
Qy	2281	GAACTTCTTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGGAGGGCGGTTTCATCC	2340
Db	2281	GAACTTCTTTCCAGGATAACTGAAGTCTTTTGACTTTTGGGGGAGGGCGGTTTCATCC	2340
Qy	2341	TCCTTCGCTTCAATAAAGTCAATTAATTTATTAAGACCTTGTGTGGCAGTTTAACTTG	2400
Db	2341	TCCTTCGCTTCAATAAAGTCAATTAATTTATTAAGACCTTGTGTGGCAGTTTAACTTG	2400
Qy	2401	CTTTCACCTATATTTTGTGTATTTTGTACTGTATGTAAGAAATTTTGTATGTAANAATA	2460
Db	2401	CTTTCACCTATATTTTGTGTATTTTGTACTGTATGTAAGAAATTTTGTATGTAANAATA	2460
Qy	2461	TAGTTATAGACCTAAATAAACTTTTAAAACTCC	2493
Db	2461	TAGTTATAGACCTAAATAAACTTTTAAAACTCC	2493

RESULT 2

AEBS4684
ID AEBS4684 standard; DNA; 2279 BP.

XX
AC AEB54684;

XX
DT 06-OCT-2005 (first entry)

DE DNA encoding human heat shock 70kDa protein 6, XX

XX
KW heat shock 70kDa protein 6; cancer; neoplasm; gene expression; diagnosis;
KW screening; drug screening; microarray; cytostatic; gene; ds.

XX Homo sapiens.

XX	Key	Location/Qualifiers
FH	CDS	110. .2041
FT		/*tag= a
FT		/product= "Heat sho
FT		

XX

WO2005067650-A2.

XX
PD 28-JUL-2005.

XX
PF 05-JAN-2005; 2005WO-US000518.

XX
PR 06-JAN-2004; 2004US-0534825P.XX
PA (FARB) BAYER PHARM CORP.

XX
PI Pauloski N, Lynch MJ, Tang L;

XX
DR WPI; 2005-542034/55.
DR P-PSDB; AEB54704.

XX Monitoring or predicting the response to anti-cancer agent comprises
 PT determining the gene expression profiles of the sample taken from the
 PT patient.
 PT

XX
PS Claim 3; SEQ ID NO 10; 91pp; English.

The invention relates to a method of monitoring or predicting the response of a patient treated for cancer by administering an anti-cancer agent. The method comprises: (a) determining the level of expression of one or more genes or gene products in a first biological sample taken from the patient prior to treatment with the anti-cancer agent; (b) determining the level of expression of one or more genes or gene products in at least a second biological sample taken from the patient subsequent to the treatment with the anti-cancer agent; and (c) comparing the level of expression of one or more genes(s) or gene products in the second biological sample with the level of expression of one or more genes(s) or gene products in the first biological sample, where a change in the level of expression of one or more genes or gene products in the second biological sample compared to the level of expression of one or more genes or gene products in the first biological sample indicates the efficacy of the treatment with the anti-cancer agent or predicts the response of the patient to anti-cancer agent. Also described are: (1) a method for identifying a compound, useful for treating cancer; (2) a method for providing a patient diagnosis for cancer; (3) a microarray comprising two or more probes corresponding to two or more genes comprising any of the 20 nucleotide sequences given as SEQ ID NOS: 1-20 in the specification or comprising two or more polypeptides comprising any of the 20 sequences given as SEQ ID NOS: 21-40 in the specification; and (4) a test kit comprising a primer or probe for measuring the expression level of a nucleic acid selected from SEQ ID NOS: 1-20 or comprising an antibody specific for a polypeptide selected from SEQ ID NOS: 21-40. Also disclosed are methods for screening the effects of a drug on a tissue or cell sample, for discovering novel drugs, for distinguishing between normal and diseases states, and for determining the phenotype of cells. The methods of the invention are useful for obtaining gene expression profiles, and microarrays comprising nucleic acid sequences representing gene expression profiles. In particular, the methods of the invention are useful for monitoring or predicting the response of a patient treated for cancer by administering an anti-cancer agent. The composition and methods are useful for diagnosing and treating cancer. This sequence represents a human polynucleotide sequence that can be used in the method of the invention.

Sequence 2279 BP; 528 A; 637 C; 711 G; 403 T; 0 U; 0 Other;

Query Match	20.1%	Score 502;	DB 14;	Length 2279;
Best Local Similarity	98.8%	Pred. No. 1.1e-232;		
Matches 142;	Conservative	0;	Mismatches 16;	Indels 1

[illegible]

194 GCCTCCGTGGCTCCAGCATCCGACAGAGCTTCAGCATGAGGGGCCACGGGAGTTC 253

Db 71 GCCTCGTGGCTCCAGCATCCGACAGAAGCTTCAGGCATGCGAGGCCCCCGGGAGTTC 130

QY 254 GCGGTGGGCATCGACCTGGGCACCACTACTCGTGGTGGGCGTGTTCAGCAGGGCGCGC 313

Db	131	CGCGTGGGCATCGACCTTGGGCACCACTTACTCTGTGCGTGGGCGTGTCTTCAGACGAGGCGCG	190
Qy	314	GTGAGATCTCTGGCCAAACGACACAGGGCAACCGCACCGCCACGCTACGTGGCCCTTCACC	373
Db	191	GTGAGATCTCTGGCCAAACGACACAGGGCAACCGCACCGCCACGCTACGTGGCCCTTCACC	250
Qy	374	GACACCGACGCGCTGGTCCGGGACCGCGCCAAAGACCGAGGCGGCGCCCTGAACCCCCCAACAAC	433
Db	251	GACACCGACGCGCTGGTCCGGGACCGCGCCAAAGACCGAGGCGGCGCCCTGAACCCCCCAACAAC	310
Qy	434	ACCGTGTTCGATGCCAAACGCGCTGATCGGGCGCAAGTTCGGGGAACAACAAGTGCAGTCG	493
Db	311	ACCGTGTTCGATGCCAAACGCGCTGATCGGGCGCAAGTTCGGGGAACAACAAGTGCAGTCG	370
Qy	494	GACATGAGCACTGGCCCTTCCAGGTGTGACGAGGGCGGCGCAAGCCCAAGGTGCGCGTA	553
Db	371	GACATGAGCACTGGCCCTTCCAGGTGTGACGAGGGCGGCGCAAGCCCAAGGTGCGCGTA	430
Qy	554	TGCTACCGCGGGAGGACAAGACGTTCTTACCCCGAGGAGATCTCGTCCATGGTCTCGAC	613
Db	431	TGCTACCGCGGGAGGACAAGACGTTCTTACCCCGAGGAGATCTCGTCCATGGTCTCGAC	490
Qy	614	AAGATGAAGGAGAAGCGCGAGGCGTACTCGGCGCAGCCCGGTGAAGCAACGATGATCACC	673
Db	491	AAGATGAAGGAGAAGCGCGAGGCGTACTCGGCGCAGCCCGGTGAAGCAACGATGATCACC	550
Qy	674	GTGCCACCTATTTTCAGTTAACTCGCAGCGCCAGCGCCACCAAGGACCGGGGCCATCGCG	733
Db	551	GTGCCCGCTATTTTCAATGACTCGCAGCGCCAGCGCCACCAAGGACCGGGGCCATCGCG	610
Qy	734	GGGCTCAAGTGTCTGCCCATCATCAATGAGGCCACGGCAGCAGCATCGCCTATGGGCTG	793
Db	611	GGGCTCAACGTTTGCAGATCATCAATGAGGCCACGGCAGCAGTGCATCGCCTATGGGCTG	670
Qy	794	GACCGCGGGCGCGGGGAAACGCAACGTGTCTCAATTTTGAACCTGGGTGGGGGCACTTTC	853
Db	671	GACCGCGGGCGCGGGGAGAGCGCAACGTGTCTCAATTTTGAACCTGGGTGGGGGCACTTTC	730
Qy	854	GATGTGTCGGTCTTCTCCATTTGAACCGCGGTGTCTTGAAGTGAAGGCACTGCTGGAGAT	913
Db	731	GATGTGTCGGTCTTCTCCATTTGAACCGTGTGTCTTGAAGTGAAGGCACTGCTGGAGAT	790
Qy	914	ACCACCTTGGAGGAGAGGACTTGCACAAACCGGCTCGTGAACCACTTCACTGAAGAAATTC	973
Db	791	ACCACCTTGGAGGAGAGGACTTGCACAAACCGGCTCGTGAACCACTTCACTGAAGAAATTC	850
Qy	974	CGCGGAAGCATGGGAAGGACCTTGACGCGGAAACAAAGCGTGCCTCGCAGGCTCGCACACA	1033
Db	851	CGCGGAAGCATGGGAAGGACCTTGACGCGGAAACAAAGCGTGCCTCGCAGGCTCGCACACA	910
Qy	1034	GCCTGTGACGCGCCCAAGCGACCCCGCTCTCAGACCCAGGCGCACCTGGAGATAGAC	1093
Db	911	GCCTGTGACGCGCCCAAGCGACCCCGCTCTCAGACCCAGGCGCACCTGGAGATAGAC	970
Qy	1094	TCCCTGTTTCGAGGGCGTGCATTTCAAGTGCATCACTCGTGCCTCGCTTTGAGGAACTG	1153
Db	971	TCCCTGTTTCGAGGGCGTGCATTTCAAGTGCATCACTCGTGCCTCGCTTTGAGGAACTG	1030
Qy	1154	TGCTCAGACCTCTTCCGCGACGACCTTGAGCGGTCGGTGGAGAGGGCCCTCGCGGATGCCAAG	1213
Db	1031	TGCTCAGACCTCTTCCGCGACGACCTTGAGCGGTCGGTGGAGAGGGCCCTCGCGGATGCCAAG	1090
Qy	1214	CTGGAACAAGGCCAGATTATGAATTCGTCTCTGGGGGAGGGCTCCACTCGCATCTCCGAA	1273
Db	1091	CTGGAACAAGGGCCAGATTATGAATTCGTCTCTGGGGGAGGGCTCCACTCGCATCTCCGAA	1149
Qy	1274	GGTCAGAAAGTGTCTGACGACTTCTTCAACGGCAAGGAGCTGACAGAGCATCAACCC	1333
Db	1150	GGTCAGAAAGTGTCTGACGAGTCTTCTTCAACGGCAAGGAGCTGACAGAGCATCAACCC	1209
Qy	1334	TGATGAGGCTGTGGCCCTATGGGTCTGTGTGCGAGCGGCCCGCTGTGTTGATGGGGGCAAAATG	1393

Db	1210	TGATGAGGCTGTGGCCCTATCTGGGGCTGTCTGTGTCAGAGCGGCGTGTGTGATGTGGGGGACAAATG	126
Qy	1394	TGACAAAGTGCAGGATCTCTCTGCTGCTGGAATGTGGCTCTCCCTCTGTCTCTGGGGCTGGAGAC	1453
Db	1270	TGAGAAAGTGCAGGATCTCTCTGCTGCTGGAATGTGGCTCTCCCTCTGTCTCTGGGGCTGGAGAC	1329
Qy	1454	AGCAGGTGGGGTGTATGACCAACGCTGTATCCAGAGGAAACGCCACCTATCCCCACCAAGCAGAC	1513
Db	1330	AGCAGGTGGGGTGTATGACCAACGCTGTATCCAGAGGAAACGCCACCTATCCCCACCAAGCAGAC	1389
Qy	1514	CCAGACTTTCACCACTTACTCTGCGACAACACGCTGGGGTCTTTCATCCAGGTGTATGAGG	1572
Db	1390	CCAGACTTTCACCACTTACTCTGCGACAACACGCTGGGGTCTTTCATCCAGGTGTATGAGG	1448
RESULT 3			
AAFI8262	ID	AAFI8262 standard; DNA; 2361 BP.	
XX	AC	AAFI8262;	
XX	DT	14-MAR-2001 (first entry)	
XX	DE	Lung cancer associated polynucleotide sequence SEQ ID 281.	
KW	XX	Human; lung cancer associated protein; neuroprotective; cytostatic;	
KW	KW	cardioactive; immunomodulatory; muscular active; vulnery;	
KW	KW	gastrointestinal; nephrotropic; antineoplastic; gynecological;	
KW	KW	antibacterial; diagnosis; neural disorder; immune disorder; reproductive;	
XX	KW	proliferative disorder; wound healing; infectious disease; ds.	
OS	XX	Homo sapiens.	
XX	PN	WO200055180-A2.	
XX	PD	21-SEP-2000.	
XX	XX	08-MAR-2000; 2000WO-US005918.	
PF	XX	12-MAR-1999; 99US-0124270P.	
PR	XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	XX	(ROSE/) ROSEN C A.	
PI	XX	Ruben SM;	
DR	XX	WPI; 2000-587514/55.	
DR	XX	P-PSDB; AAB58386.	
PT	XX	Lung cancer associated gene sequences, referred to as lung cancer	
PT	XX	antigens, useful for treatment, prevention, and diagnosis of disorders	
PT	XX	such as lung cancer.	
PS	XX	Claim 1; Page 740-741; 1425pp; English.	
CC	XX	Polynucleotide sequences AAFI7982 - AAFI8424 encode human lung cancer	
CC	CC	associated proteins represented in AAB58106 - AAB58548. Lung cancer	
CC	CC	antagonists may have neuroprotective; cytostatic; cardioactive; and	
CC	CC	immunomodulatory; muscular active general; vulnery; gastrointestinal	
CC	CC	general; nephrotropic; antineoplastic; gynecological; or antibacterial	
CC	CC	activity. The invention also includes antibodies specific for the protein	
CC	CC	or polynucleotide sequences. The lung cancer associated polynucleotide	
CC	CC	sequences may be used for detection of lung cancer, chromosome	
CC	CC	identification, as chromosome markers, and for numerous other diagnostic	
CC	CC	or research purposes. The proteins may be used to treat disorders such as	
CC	CC	neural, immune, muscular, reproductive, gastrointestinal, pulmonary,	
CC	CC	cardiovascular, renal, and proliferative disorders. The proteins may also	
CC	CC	be used in the treatment of wounds and infectious diseases.	
CC	CC	Polynucleotide sequences AAFI8425 - AAFI8433 and peptide AAB58549 are	
CC	CC	used in the course of the invention for the identification and	
CC	CC	characterisation of the polynucleotide and protein sequences	

SQ Sequence 2361 BP; 544 A; 656 C; 743 G; 410 T; 0 U; 8 Other;
Query Match 19.9%; Score 495; DB 3; Length 2361;
Best Local Similarity 99.8%; Pred. No. 2.8e-229;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 134 GCAGAGAACCGCAGGAGAGAGCTCTACTGTGAGCGCCCTCGACGGCGAGCGGACGCA 193
DB 72 GCAGAGAACCGCAGGAGAGAGCTCTACTGTGAGCGCCCTCGACGGCGAGCGGACGCA 131
QY 194 GCCTCGGTGCGCTCCAGCATCCGACAGAGCTTCAGCCATGACAGCCCGCCAGCGGAGCTC 253
DB 132 GCCTCGGTGCGCTCCAGCATCCGACAGAGCTTCAGCCATGACAGCCCGCCAGCGGAGCTC 191
QY 254 GCGGTGGGCATCGACCTGGGCACACCTACTCGTGGCGTGGCGCTGTTCAGCAGGCGCCG 313
DB 192 GCGGTGGGCATCGACCTGGGCACACCTACTCGTGGCGTGGCGCTGTTCAGCAGGCGCCG 251
QY 314 GTGGAGATCTTGGCCAAACGACGAGGGCAACCGCACCGCCAGCTACGTGGCTTTCAAC 373
DB 252 GTGGAGATCTTGGCCAAACGACGAGGGCAACCGCACCGCCAGCTACGTGGCTTTCAAC 311
QY 374 GACACGAGCGGCTGTGCGGGACGGCCCAAGACCGACCGCGCTTCAACCCCAAC 433
DB 312 GACACGAGCGGCTGTGCGGGACGGCCCAAGACCGACCGCGCTTCAACCCCAAC 371
QY 434 ACCGTGTTGATGCCAAGCGGCTGTGCGGGCAAGTTTCGCGACACCGTGCAGTGC 493
DB 372 ACCGTGTTGATGCCAAGCGGCTGTGCGGGCAAGTTTCGCGACACCGTGCAGTGC 431
QY 494 GACATGAAGCACTGGGCCCTTCCAGGTGTTGAGCGAGGGCGCAAGCCCAAGTGCAGCTA 553
DB 432 GACATGAAGCACTGGGCCCTTCCAGGTGTTGAGCGAGGGCGCAAGCCCAAGTGCAGCTA 491
QY 554 TGCCTACGCGGGGAGGACAGAGCTTCTACCCCGAGAGATCTCGTCAATGTGCTGAGC 613
DB 492 TGCCTACGCGGGGAGGACAGAGCTTCTACCCCGAGAGATCTCGTCAATGTGCTGAGC 551
QY 614 AAGATGAAGGAGACGCGCGAGGCGTACCTGGGCGACCGCTGAAGCAGCAGTGAATCACC 673
DB 552 AAGATGAAGGAGACGCGCGAGGCGTACCTGGGCGACCGCTGAAGCAGCAGTGAATCACC 611
QY 674 GTGCCC 679
DB 612 GTGCCC 617

RESULT 4

ID ADE77038 standard; cDNA; 2336 BP.
XX

AC ADE77038;
XX

DT 29-JAN-2004 (first entry)
XX

DE Human cDNA differentially expressed in a liver disorder #147.
XX

KW human; ss; gene; liver disorder; hyperlipidaemia; hypertension;
KW type II diabetes; tumour; liver; inflammatory disorder;
KW immune response disorder; high-throughput screening;
KW differential gene expression; gene therapy.
XX

OS Homo sapiens.
XX

XX US2003108871-A1.
XX

PN 12-JUN-2003.
XX

XX 30-JUL-2001; 2001US-00919039.
XX

XX 28-JUL-2000; 2000US-0222113P.
XX

XX (KASE/) KASER M R.
XX

XX Kaser MR;
XX

PI WPI: 2004-031227/03.
DR P-PSDB; ADE77039.
XX

PT Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX

PS Claim 1; SEQ ID NO 203; 41pp; English.
XX

CC The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents a cDNA
CC differentially expressed in a liver disorder.
XX

SQ Sequence 2336 BP; 515 A; 651 C; 724 G; 446 T; 0 U; 0 Other;
XX

Query Match 19.4%; Score 484; DB 12; Length 2336;
Best Local Similarity 98.8%; Pred. No. 6.1e-224;
Matches 1404; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
XX

QY 152 GAGCCTCACTGCTGAGCGCCCTCGACGGCGAGCGGAGCAGCTCGTGGCTCCAGC 211
DB 29 GAGCCTCACTGCTGAGCGCCCTCGACGGCGAGCGGAGCAGCTCGTGGCTCCAGC 88

QY 212 ATCCGACAAGAGCTTTCAGCCATGACAGGCCCCACCGGAGCTCGCGTGGGATCGACCTG 271
DB 89 ATCCGACAAGAGCTTTCAGCCATGACAGGCCCCACCGGAGCTCGCGTGGGATCGACCTG 148

QY 272 GGCACCACTACTCGTGGTGGCGCTGTTTCAGCAGGGCGCGTGGAGATCTTGGCCCAAC 331
DB 149 GGCACCACTACTCGTGGTGGCGCTGTTTCAGCAGGGCGCGTGGAGATCTTGGCCCAAC 208

QY 332 GACACGGGCAACCGCACCGCCAGCTACGTGGCTTTCACCGACACCGAGCGCTGGTTC 391
DB 209 GACACGGGCAACCGCACCGCCAGCTACGTGGCTTTCACCGACACCGAGCGCTGGTTC 268

QY 392 GGGGACGCGGCCAAGAGCCAGCGCCCTCGTGAACCCCAACACCGTGTTCGATGCCAAG 451
DB 269 GGGGACGCGGCCAAGAGCCAGCGCGCCCTCGTGAACCCCAACACCGTGTTCGATGCCAAG 328

QY 452 CGGCTGATCGGGCGCAAGTTTCGCGACACCGCTGCGAGTGGGATGAGCAGCTGGGCC 511
DB 329 CGGCTGATCGGGCGCAAGTTTCGCGACACCGCTGCGAGTGGGATGAGCAGCTGGGCC 388

QY 512 TTCCAGGTGGTGAAGCGAGGGCGGCAAGCCCAAGGTGGCGCTATGCTACCGGGGAGGAC 571
DB 389 TTCCAGGTGGTGAAGCGAGGGCGGCAAGCCCAAGGTGGCGCTATGCTACCGGGGAGGAC 448

QY 572 AAGACGTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGCAAGATGAAGAGACGCGCC 631
DB 449 AAGACGTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGCAAGATGAAGAGACGCGCC 508

QY 632 GAGGCGTACCTGGGCGACGCCCGTGAAGCAGCAGTGAATCAGCTGCCACCTATTTCACT 691
DB 509 GAGGCGTACCTGGGCGACGCCCGTGAAGCAGCAGTGAATCAGCTGCCACCTATTTCACT 568

Qy 692 AACTCGAGCGCCAGGCCACCAAGACGCGGGGGCCATCGCGGGGCTCAAGTGTCTCCG 751
Db |||||
Qy 569 GACTCGAGCGCCAGGCCACCAAGACGCGGGGGCCATCGCGGGGCTCAAGTGTCTCCG 628
Db |||||
Qy 752 ATCATCAATGAGGCCACCGCAGAGCCATCGCTATGGGCTGGACCGCGGGGGCGCGGA 811
Db |||||
Qy 629 ATCATCATGAGCCACCGCAGCTGCCATCGCTATGGGCTGGACCGCGGGGGCGCGGA 688
Db |||||
Qy 812 AAGCGCAACGTCTCATTTTTGA CTTGGGTGGGGGCACTTCGATGTCTCGTTCTCTCC 871
Db |||||
Qy 689 GAGCGCAACGTCTCATTTTTGA CTTGGGTGGGGGCACTTCGATGTCTCGTTCTCTCC 748
Db |||||
Qy 872 ATTGACCGCGTGTCTTTGAGGTGAAGCCACTGCTGAGATACCCACTGGAGGAG 931
Db |||||
Qy 749 ATTGACGCTGTGTCTTTGAGGTGAAGCCACTGCTGAGATACCCACTGGAGGAG 808
Db |||||
Qy 932 GACTTCGACAACCGGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 991
Db |||||
Qy 809 GACTTCGACAACCGGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 868
Db |||||
Qy 992 GACTTCGAGCGGGAACAAGCGTGCCTCGCAGGCTGCGCAAGCTGTGAGGCGGCCAAG 1051
Db |||||
Qy 869 GACTTCGAGCGGGAACAAGCGTGCCTCGCAGGCTGCGCAAGCTGTGAGGCGGCCAAG 928
Db |||||
Qy 1052 CGCACCCCGTCTCCAGCACCCAGCCACCTGGAGATAGACTCCCTGTTTCGAGGGCGTG 1111
Db |||||
Qy 929 CGCACCCCGTCTCCAGCACCCAGCCACCTGGAGATAGACTCCCTGTTTCGAGGGCGTG 988
Db |||||
Qy 1112 GACTTCTACAAAGTCCATCACTCGTCCCGCTTTTGAGGAACCTGTGCTCAGACCTCTTCCGC 1171
Db |||||
Qy 989 GACTTCTACAGTCCATCACTCGTCCCGCTTTTGAGGAACCTGTGCTCAGACCTCTTCCGC 1048
Db |||||
Qy 1172 AGCACCTTGAGCGCGGTGAGAAAGCCCTGCGGGATGCCAAGCTGGACAAGGCCCAGATT 1231
Db |||||
Qy 1049 AGCACCTTGAGCGCGGTGAGAAAGCCCTGCGGGATGCCAAGCTGGACAAGGCCCAGATT 1108
Db |||||
Qy 1232 CATGACTTCGCTCGGGGGGGGCTCCACTCGCATCCCAAGTGGCAGAGTGTGCTGCA 1291
Db |||||
Qy 1109 CATGACTTCGCTCGTGTGGG -GGGCTCCACAGCATCCCAAGTGGCAGAGTGTGCTGCA 1167
Db |||||
Qy 1292 GGACTTCTTCAACGGCAAGGAGCTGAACAAGAGCATCAACCTCGATGAGGCTGTGGCCTA 1351
Db |||||
Qy 1168 GGACTTCTTCAACGGCAAGGAGCTGAACAAGAGCATCAACCTCGATGAGGCTGTGGCCTA 1227
Db |||||
Qy 1352 TGGGCTGCTGTGAGAGCGCGCTGTGATGAGGGGACAAATGTGAGAAAGTGCAGGATCT 1411
Db |||||
Qy 1228 TGGGGCTGTGTGACAGCGCGCGCTGTGATGAGGGGACAAATGTGAGAAAGTGCAGGATCT 1287
Db |||||
Qy 1412 CCTGCTGTGATGTGGGCTCCCTCTCTCTGGGGCTGGAGACAGCAGGTGGGTTGATGAC 1471
Db |||||
Qy 1288 CCTGCTGTGATGTGGGCTCCCTCTCTCTGGGGCTGGAGACAGCAGGTGGGTTGATGAC 1347
Db |||||
Qy 1472 CACGCTGATCCAGAGGAACGCGCACTATCCCAACCAAGCAGACCCAGACTTTTCAACACCTA 1531
Db |||||
Qy 1348 CACGCTGATCCAGAGGAACGCGCACTATCCCAACCAAGCAGACCCAGACTTTTCAACACCTA 1407
Db |||||
Qy 1532 CTCGAGCAACAGCTGGGCTTTCATTCAGGTGTATGAGG 1572
Db |||||
Qy 1408 CTCGAGCAACAGCTGGGCTTTCATTCAGGTGTATGAGG 1448
Db |||||

RESULT 5

ABX62981
ID ABX62981 standard; cDNA; 2962 BP.
XX
XX
AC ABX62981;
XX
XX
DT 25-FEB-2003 (first entry)
XX
XX
DE Human activated T cell cDNA #97.
XX
XX
KW T cell; gene; ss; differential expression; T cell activation;
KW antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy;

KW allergy; cancer; graft versus host disease; infection;
KW autoimmune disorder.
XX
XX Homo sapiens.
OS
XX
XX US2002137077-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 25-OCT-2001; 2001US-00002600.
PF
XX
XX 25-OCT-2000; 2000US-0243521P.
PR
XX
XX (HOPK/) HOPKINS C M.
PA (PETE/) PETERSON D P.
PA (COCK/) COCKS B G.
PA (HAWK/) HAWKINS P R.
XX
XX
XX Hopkins CM, Peterson DP, Cocks BG, Hawkins PR;
PI
XX
XX WPI; 2003-102381/09.
DR
XX
XX
PT New combination comprising several cDNAs that are differentially
PT expressed in activated T cells, useful for diagnosing, treating, staging
PT or monitoring treatment for allergy, cancer, infectious and/or autoimmune
PT disorders.
PT
XX
XX Claim 1; Page; 180pp; English.
PS
XX
XX This invention relates to the sequences of several cDNAs that are
XX differentially expressed in activated T cells. The sequences of the
XX invention may have antiallergic, cytostatic, immunosuppressive and
XX antimicrobial activity and may be used in gene therapy. The invention
XX also comprises a method for screening samples for differentially
XX expressed genes and a method for detecting these cDNAs by hybridisation.
XX The methods and compositions of the present invention are useful for
XX diagnosing, treating, staging or monitoring treatment for allergy,
XX cancer, chronic graft versus host disease, infectious and/or autoimmune
XX disorders. The present sequence represents a cDNA of the invention that
XX is differentially expressed in activated T cells
SQ
Sequence 2962 BP; 643 A; 837 C; 909 G; 573 T; 0 U; 0 Other;
Query Match 17.3%; Score 431; DB 8; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.3e-198;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 198 CCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCAGGCCCCACGGGAGCTCGCG 257
Db |||||
Qy 699 CCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCAGGCCCCACGGGAGCTCGCG 758
Db |||||
Qy 258 TGGGCATCGACCTGGGCACCACTTACTCTGCTGGGGGTGTTTCAGCAGGGCGCGTGG 317
Db |||||
Qy 759 TGGGCATCGACCTGGGCACCACTTACTCTGCTGGGGGTGTTTCAGCAGGGCGCGTGG 818
Db |||||
Qy 318 AGATCTCTGGCCAAACGACGAGGCAACCGCACCGCCAGCTAGTGGCTTCACCGACA 377
Db |||||
Qy 819 AGATCTCTGGCCAAACGACGAGGCAACCGCACCGCCAGCTAGTGGCTTCACCGACA 878
Db |||||
Qy 378 CCGAGCGGCTGGTGGGGGACGCGGCCCAAGAGCCAGGGCGCCCTGAACCCCCACACACG 437
Db |||||
Qy 879 CCGAGCGGCTGGTGGGGGACGCGGCCCAAGAGCCAGGGCGCCCTGAACCCCCACACACG 938
Db |||||
Qy 438 TGTTCGATGCCAAGCGGCTGATTCGGGGCGCAAGTTCGGGGACACACCGTGCAGTCGGACA 497
Db |||||
Qy 939 TGTTCGATGCCAAGCGGCTGATTCGGGGCGCAAGTTCGGGGACACACCGTGCAGTCGGACA 998
Db |||||
Qy 498 TGAAGCACTGGCCTTCAGAGTGTGAGCGAGGGCGGCAAGCTGCGCGTATGCT 557
Db |||||
Qy 999 TGAAGCACTGGCCTTCGGGGTGTGAGCGAGGGCGGCAAGCTGCGCGTATGCT 1058
Db |||||
Qy 558 ACCCGGGGAGCAAGAAGCTTCTACCCGAGGAGATCTCGTCCATGCTGTGAGCAAGA 617
Db |||||


```
Db 1059 ACCGCGGGAGGACAGACGCTTACCCCGAGGAGATCTCGTCCATGCTGAGCAAGA 1118
Qy 618 TGAAGGAGACGGCGAGCGCTACTCTGGGCGAGCCCGTGAAGCAGCAGTGTATCACCGTGC 677
Db 1119 TGAAGGAGACGGCGAGCGCTACTCTGGGCGAGCCCGTGAAGCAGCAGTGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 6
ADI61704
ID ADI61704 standard; cDNA; 2962 BP.
XX
AC ADI61704;
DT 16-DEC-2004 (first entry)
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 349676.8.
XX
KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
KW brain disorder.
XX
OS Homo sapiens.
XX
PN US6682888-B1.
XX
PD 27-JAN-2004.
XX
PF 05-MAY-2000; 2000US-00566921.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
PI Loring JF, Tingley DW, Edwards CM;
XX
DR WPI; 2004-118572/12.
XX
PT New composition comprising cDNAs that are differentially expressed in
PT brain disorders, useful for diagnosing or treating Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 72; 223pp; English.
XX
CC The invention relates to a new composition comprising ADI61633-
CC ADI61704 and their complements that are cDNAs differentially expressed in
CC brain disorders. Also included are a high throughput method for detecting
CC differential expression of one or more cDNAs in a sample containing
CC nucleic acids and a high throughput method for screening a library of
CC molecules or compounds to identify a ligand that specifically binds a
CC cDNA. The expression of the each of the cDNAs is downregulated at least
CC two-fold in the brain of the subjects with Alzheimer's disease (ADI61633-
CC ADI61727) or upregulated at least two fold in Alzheimer's disease
CC (ADI61728-ADI6170). The composition is useful for diagnosing or treating
CC Alzheimer's disease. The present sequence is a cDNA downregulated at
CC least two-fold in the brain of the subjects with Alzheimer's disease.
XX
SQ Sequence 2962 BP; 641 A; 838 C; 909 G; 574 T; 0 U; 0 Other;

Query Match 17.3%; Score 431; DB 13; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.3e-198;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CGGTGCTCCAGATCCACAGAGCTTCAGCCATGAGGCCCCACCGGAGCTCGCGG 257
Db 699 CGGTGCTCCAGATCCACAGAGCTTCAGCCATGAGGCCCCACCGGAGCTCGCGG 758
Qy 258 TGGGATCGACCTGGGCGCACCTACTCTGTGGTGGCGGTGTTTCAGCAGGCGCGGTGG 317
Db 759 TGGGATCGACCTGGGCGCACCTACTCTGTGGTGGCGGTGTTTCAGCAGGCGCGGTGG 818
Qy 318 AGATCTGGCCAAACGACGAGGGGCAACCGCACCGCCAGCTACGTGGCGCTTTCACCGACA 377
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Db 819 AGATCTGGCCAAACGACGAGGSCAACCGCACCAAGCCAGCTACGTGGCGCTTTCACCGACA 878
Qy 378 CCGAGGCGCTGGTTCGGGGAGCGGGCCCAAGAGCAGCGGCGCCCTGAAACCCCCCAACAACCG 437
Db 879 CCGAGGCGCTGGTTCGGGGAGCGGGCCCAAGAGCAGCGGCGCCCTGAAACCCCCCAACAACCG 938
Qy 438 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTTCGCGGACACACCGGTGCGAGTCCGACA 497
Db 939 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTTCGCGGACACACCGGTGCGAGTCCGACA 998
Qy 498 TGAAGCACTGGCCCTTCCAGGTGGTGAAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCT 557
Db 999 TGAAGCACTGGCCCTTCCAGGTGGTGAAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCT 1058
Qy 558 ACCGCGGGGAGGACAGAGCTTCTACCCCGAGGAGATCTCGTCCATGCTGCTGAGCAAGA 617
Db 1059 ACCGCGGGGAGGACAGAGCTTCTACCCCGAGGAGATCTCGTCCATGCTGCTGAGCAAGA 1118
Qy 618 TGAAGGAGACGGCGAGGCGTACCTGGGCGCAGCCCGTGAAGCAGCAGTGTATCACCGTGC 677
Db 1119 TGAAGGAGACGGCGAGGCGTACCTGGGCGCAGCCCGTGAAGCAGCAGTGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 7
AEA43869
ID AEA43869 standard; cDNA; 2962 BP.
XX
AC AEA43869;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human cDNA differentially expressed in brain tissue SEQ ID NO:72.
XX
KW diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
KW muscular-gen.; cytosolic; neuroleptic; nootropic; antidepressant;
KW anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
KW immunotherapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN US2005130171-A1.
XX
PD 16-JUN-2005.
XX
PF 26-JAN-2004; 2004US-00765700.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
PI Loring JF, Tingley DW, Edwards CM;
XX
DR WPI; 2005-456990/46.
XX
PT Composition useful for diagnosis, staging, treating or monitoring
PT treatment of a subject with a brain disorder, comprises several cDNAs
PT that are differentially expressed in brain disorders.
XX
PS Claim 1; SEQ ID NO 72; 231pp; English.
XX
CC The invention relates to a composition (I) for the diagnosis, staging,
CC treatment or for the monitoring of treatment of a subject with a brain
CC disorder. (I) comprises several cDNAs that are differentially expressed
CC in brain disorders and chosen from any one of 138 nucleotide sequences of
CC AEA43798-AEA43935, or their complements. Also described: (1) a high
CC throughput method for detecting differential expression of one or more
CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
CC selected from AEA43812, AEA43813, AEA43830, AEA43851, AEA43855, AEA43856,
```

CC AEA43983 and AEA43923; (3) an expression vector (III) containing (II);
CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
CC for a high throughput method of screening a library of molecules or
CC compounds to identify a ligand which specifically binds a cDNA, where the
CC method involves combining (I) with the library of molecules or compound
CC under conditions to allow specific binding and detecting specific binding
CC between each cDNA and a molecule or compound. (IV) is useful for
CC producing a protein, which involves culturing (IV) under conditions for
CC the expression of the protein and recovering the protein from the
CC culture. (V) is useful for high throughput method for screening a library
CC of molecules or compounds to identify a ligand which specifically binds
CC (V), where the method involves combining (V) or its portion with the
CC library of molecules or compound under conditions to allow specific
CC binding and detecting specific binding between (V) and a molecule or
CC compound. (V) is useful for purifying a ligand from a sample, which
CC involves combining (V) or its portion with the sample under conditions to
CC allow specific binding, recovering the bound protein and separating the
CC protein from ligand. (V) is also useful for producing an antibody which
CC involves immunizing an animal with (V) or its portion under conditions to
CC elicit an antibody response, isolating animal antibodies and screening
CC the isolated antibodies with the protein. (II) is useful in gene therapy
CC for the treatment or prevention of conditions and disorders associated
CC with immune response. The present sequence represents a human cDNA
CC sequence which is differentially expressed in brain tissues, which is
CC used in the exemplification of the present invention.

XX SQ Sequence 2962 BP; 641 A; 838 C; 909 G; 574 T; 0 U; 0 Other;

Query Match 17.3%; Score 431; DB 14; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.3e-198;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATCAGGCCCCACGGAGCTCGCG 257
Db 699 CGGTGGCTCCAGCATCCGACAAAGCTTCAGCCATCAGGCCCCACGGAGCTCGCG 758
Qy 258 TGGGATCGACTGGGACACCTACTCTGTGGTGGGGGTGTTTCAGCAGGGCCGCGTGG 317
Db 759 TGGGATCGACTGGGACACCTACTCTGTGGTGGGGGTGTTTCAGCAGGGCCGCGTGG 818
Qy 318 AGATCTGGCCAAACGACGAGGCAACCCGACCCAGCTACGTGGCCCTTACCCGACA 377
Db 819 AGATCTGGCCAAACGACGAGGCAACCCGACCCAGCTACGTGGCCCTTACCCGACA 878
Qy 378 CCGAGCGCTGTGTGGGACGCGGCCAAGAGCGCAGGCGGCCCTGAAACCCCCACACACCG 437
Db 879 CCGAGCGCTGTGTGGGACGCGGCCAAGAGCGCAGGCGGCCCTGAAACCCCCACACACCG 938
Qy 438 TGTTCGATCCGACGCGCTGATCGGGCGCAAGTTCCGCGACACACGTCAGTCGCGACA 497
Db 939 TGTTCGATCCGACGCGCTGATCGGGCGCAAGTTCCGCGACACACGTCAGTCGCGACA 998
Qy 498 TGAACACTGGCCCTTCCAGGTGGTGAGCGAGGGCGGCAAGCCCAAGTGGCGGTATGCT 557
Db 999 TGAACACTGGCCCTTCCAGGTGGTGAGCGAGGGCGGCAAGCCCAAGTGGCGGTATGCT 1058
Qy 558 ACCCGGGGAGGACAAAGAGTGTCTACCCCGAGGAGATCTCGTCCATGTGTGAGCAAGA 617
Db 1059 ACCCGGGGAGGACAAAGAGTGTCTACCCCGAGGAGATCTCGTCCATGTGTGAGCAAGA 1118
Qy 618 TGAAGGACGCGCCGAGCGTACTTGGGCGAGCCCGTGAAGCAGCAGTATCACCGTGC 677
Db 1119 TGAAGGACGCGCCGAGCGTACTTGGGCGAGCCCGTGAAGCAGCAGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 8
ADP66225/c
ID ADP66225 standard; cDNA; 531 BP.

XX AC ADP66225;
XX DT 26-AUG-2004 (first entry)
XX DE Human cDNA from gene modulated by pro-inflammatory cytokines #45.
XX KW Human; se; cytokine; peripheral blood mononuclear cell; PBMC;
KW differential expression; immune disorder; pro-inflammatory disorder;
KW viral infection; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; multiple sclerosis;
KW encephalomyelitis; inflammatory bowel disease; psoriasis;
KW pemphigus vulgaris; anti-inflammatory disorder; bacterial infection;
KW parasitic infection; allergy; topic disorder;
KW chronic graft-versus-host disease; scleroderma;
KW systemic lupus erythematosus; probe.
XX OS Homo sapiens.
XX PN US2004110194-A1.
XX PD 10-JUN-2004.
XX PF 07-AUG-2003; 2003US-00637855.
XX PR 05-NOV-1999; 99US-00435247.
XX PA (INCY-) INCYTE CORP.
XX PI Sornasse T, Cocks BG, Sanjawala B;
XX DR WPI; 2004-486580/46.
XX PT A composition comprises polynucleotides that are modulated in response to
PT cytokines, useful for diagnosing or treating conditions associated with
PT an immune response, e.g. infection, diabetes, allergies or scleroderma.
XX PS Claim 1; SEQ ID NO 217; 210pp; English.
XX CC The invention relates to a composition comprising polynucleotides whose
CC expression is modulated by cytokines, where the polynucleotides comprise
CC any of the cDNA fragments (isolated from peripheral blood mononuclear
CC cells (PBMC)) and appearing as ADP66009-ADP66524, or their complements.
CC Also included are a substantially purified polynucleotide whose
CC expression is modulated by cytokines comprising at least a fragment of a
CC gene selected from ADP66009-ADP66251, a high throughput method for
CC detecting a polynucleotide in a sample, methods of purifying ligands, an
CC expression vector containing the above polynucleotide, a host cell
CC containing the expression vector, a method for producing a protein, a
CC protein or its portion produced by the method, high throughput methods of
CC screening a library of molecules or compounds to identify a ligand or at
CC least one ligand which specifically binds a protein, and a method of
CC screening a sample from a patient for an immune response, disorder,
CC condition or disease. The immune disorder, condition or disease is a pro-
CC inflammatory disorder (selected from viral infections, rheumatoid
CC arthritis, insulin-dependent diabetes mellitus, multiple sclerosis,
CC encephalomyelitis, inflammatory bowel disease, psoriasis, and pemphigus
CC vulgaris) and an anti-inflammatory disorder (selected from bacterial and
CC parasitic infections, allergies and other topic disorders, chronic graft-
CC versus-host disease, scleroderma and systemic lupus erythematosus). The
CC composition and methods are useful for detecting genes modulated in
CC response to human cytokines or for diagnosing useful for diagnosing or
CC treating conditions associated with an immune response. The present
CC sequence is a cDNA fragment from a gene whose expression is modulated by
CC pro-inflammatory cytokines. NOTE: Details of the expression levels of the
CC genes in response to various cytokines are said to be contained in tables
CC 1-4, but these tables are not included in the specification.
XX SQ Sequence 531 BP; 151 A; 141 C; 118 G; 121 T; 0 U; 0 Other;

Query Match 17.2%; Score 429; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 3e-197;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2024	GGAGCTGGAGCAAACTGTGCGCCCATCTTCTCAGGCTCTATGGGGGGGCGCTGGTGTCCC	2083
Db	429	GGAGCTGGAGCAAACTGTGCGCCCATCTTCTCAGGCTCTATGGGGGGGCGCTGGTGTCCC	370
Qy	2084	TGGGGGCGAGCAGTTGTAGCGCTCAAGGCCACACAGGGGGACCCGACGACCGGGCCCCATCAT	2143
Db	369	TGGGGGCGAGCAGTTGTAGCGCTCAAGGCCACACAGGGGGACCCGACGACCGGGCCCCATCAT	310
Qy	2144	TGAGGAGTTGATTTGAATGCGCCCTTCCTGATAGTCAGCTGTGACTGTGAGGGCTATGCT	2203
Db	309	TGAGGAGTTGATTTGAATGCGCCCTTCCTGATAGTCAGCTGTGACTGTGAGGGCTATGCT	250
Qy	2204	ATGGGCGTTCTAGACTGTCTTCTATGATCCTGCCCTTCAGAGATGAAGGGCTTGGGGGGG	2263
Db	249	ATGGGCGTTCTAGACTGTCTTCTATGATCCTGCCCTTCAGAGATGAAGGGCTTGGGGGGG	190
Qy	2264	TCCTTCCCTCCAAAGCTAGAACTTCTTTCCAGAGTAACTAAGCTTTTGACATTTTGGG	2323
Db	189	TCCTTCCCTCCAAAGCTAGAACTTCTTTCCAGAGTAACTAAGCTTTTGGCTTTTGGG	130
Qy	2324	GGGAGGCGGTTCATCCTCTCTGCTTCAAATAAAAAGTCATTAATTTATTAATAACTTGT	2383
Db	129	GGGAGGCGGTTCATCCTCTCTGCTTCAAATAAAAAGTCATTAATTTATTAATAACTTGT	70
Qy	2384	GTGCGACTTTAAACATTTGCTTTCCACTATATTTTGTGTAATTTTGTCTACTGTATGTATGAA	2443
Db	69	GTGCGACTTTAAACATTTGCTTTCCACTATATTTTGTGTAATTTTGTCTACTGTATGTATGAA	10
Qy	2444	TTTTGTTAT	2452
Db	9	TTTTGTTAT	1

RESULT 9

ABL68660

ID	ABL68660 standard; DNA; 2492 BP.
XX	
XX	ABL68660;
AC	
XX	
XX	15-MAY-2002 (first entry)
DT	
XX	
XX	Kidney cancer related gene sequence SEQ ID NO:6997.
DE	
XX	
XX	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.

OS Homo sapiens.

XX PN WO200194629-A2.

PD 13-DEC-2001.

30-MAY-2001: 2001WO-US010838.

PR 05-JUN-2000; 2000US-0209473P;

PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.

PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.

PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.

PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.

PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.

PR 26-SEP-2000; 2000US-0235637P.

PR	26-SEP-2000;	2000US-0235538P;
PR	27-SEP-2000;	2000US-0235711P;
PR	27-SEP-2000;	2000US-0235720P;
PR	27-SEP-2000;	2000US-0235840P;
PR	27-SEP-2000;	2000US-0235863P;
PR	28-SEP-2000;	2000US-0236028P;
PR	28-SEP-2000;	2000US-0236032P;
PR	28-SEP-2000;	2000US-0236033P;
PR	28-SEP-2000;	2000US-0236034P;
PR	28-SEP-2000;	2000US-0236109P;
PR	28-SEP-2000;	2000US-0236111P;
PR	29-SEP-2000;	2000US-0236842P;
PR	29-SEP-2000;	2000US-0236891P;
PR	02-OCT-2000;	2000US-02371172P;
PR	02-OCT-2000;	2000US-02371173P;
PR	02-OCT-2000;	2000US-0237278P;
PR	02-OCT-2000;	2000US-0237294P;
PR	02-OCT-2000;	2000US-0237295P;
PR	02-OCT-2000;	2000US-0237316P;
PR	03-OCT-2000;	2000US-0237425P;
PR	03-OCT-2000;	2000US-0237598P;
PR	03-OCT-2000;	2000US-0237604P;
PR	03-OCT-2000;	2000US-0237606P;
PR	03-OCT-2000;	2000US-0237658P;
PR	01-NOV-2000;	2000US-0244867P;
PR	01-NOV-2000;	2000US-0244867P;
PR	01-NOV-2000;	2000US-0244868P;
PR	01-NOV-2000;	2000US-0245084P;

PA (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S
PI Soppet DR, Weaver Z;
XX WPI; 2003-188264/24.
DR

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

Sequence 2492 BP: 553 A: 683 C: 790 G: 466 T: 0 U: 0 Other: 0

Query Match 13.2%; Score 329; DB 6; Length 2492;
Best Local Similarity 100.0%; Pred NC 1 1e-148.

Q17 GGAGCAGCCTCCCTGGCTCCAGCATCCGACAGAAGCTTCAGCCATGCAGGCCCCACG 246

QY 247 GGAGCTCGGGGTGGGCATCGACCTGGGGCACCACCTACTCGTGGTGGGCGGTGTTTCAGCA 306

307 GGGCCGGTGGAGATCCTGGCCACGACAGGGCAACCGCACCGCCAGCTACGTGGC 366

Db 325 GGGCGCGTGGAGATCTTGGCCNAGACACCGGGACACCGACCGCCACCTAGCTGGC 384
Qy 367 CTTACACGACACCGAGCGGCTGGTGGGGAACCGGCCAAGAGCCAGCGGCCCTGAACCC 426
Db 385 CTTACACGACACCGAGCGGCTGGTGGGGAACCGGCCAAGAGCCAGCGGCCCTGAACCC 444
Qy 427 CCACACACCGTGTTCGATGCCAGCGGCTGATCGGGGCGCAAGTTCGGGACACCAACGGT 486
Db 445 CCACACACCGTGTTCGATGCCAGCGGCTGATCGGGGCGCAAGTTCGGGACACCAACGGT 504
Qy 487 CGAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 CGAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 10

ABK84553

ID ABK84553 standard; cDNA; 2492 BP.

XX AC ABK84553;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #1124.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.

XX OS Homo sapiens.

XX PN WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX PS WPI; 2002-435328/46.

XX PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.

XX PS Claim 1; SEQ ID NO 1124; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2492 BP; 553 A; 683 C; 790 G; 466 T; 0 U; 0 Other;

Query Match 13.2%; Score 329; DB 6; Length 2492;
Best Local Similarity 100.0%; Pred. No. 1.1e-148;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGAGCCTCCGTGGCCTCCAGCATCCGACAAAGAAGCTTCAGCCATGAGGCCCCACG 246
Db 205 GGCAGAGCCTCCGTGGCCTCCAGCATCCGACAAAGAAGCTTCAGCCATGAGGCCCCACG 264
Qy 247 GGAGCTCGGTGGGATCGACCTGGGCACCACTACTCTGTCGTGGCGGTGTTTCAGCA 306
Db 265 GGAGCTCGGTGGGATCGACCTGGGCACCACTACTCTGTCGTGGCGGTGTTTCAGCA 324
Qy 307 GGGCCGCGTGAGATCCTGGCCAAACGACAGGGCAACCGCACCGCCAGCTACGTGGC 366
Db 325 GGGCCGCGTGAGATCCTGGCCAAACGACAGGGCAACCGCACCGCCAGCTACGTGGC 384
Qy 367 CTTACCGACACCGAGCGGCTGGTGGGGAGCGGGCCAAAGCGGGCCCTGNAACCC 426
Db 385 CTTACCGACACCGAGCGGCTGGTGGGGAGCGGGCCAAAGCGGGCCCTGNAACCC 444
Qy 427 CCACACACCGTGTTCGATGCCAGCGGCTGATCGGCGCAAGTTCGGCGACACCAACGGT 486
Db 445 CCACACACCGTGTTCGATGCCAGCGGCTGATCGGCGCAAGTTCGGCGACACCAACGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 11

ACA64921

ID ACA64921 standard; DNA; 2492 BP.

XX AC ACA64921;

XX DT 27-JUN-2003 (first entry)

XX DE Human HSP70B DNA corresponding to X51757.

XX KW Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.

XX OS Homo sapiens.

XX PN DE10127572-A1.

XX PD 05-DEC-2002.

XX PF 30-MAY-2001; 2001DE-01027572.

XX

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PR 30-MAY-2001; 2001DE-01027572.
XX (PATH-) PATHOARRAY GMBH.
XX Haeupl T, Ungethuen U, Blaess S;
XX WPI; 2003-240797/24.
XX
XX Reagents for diagnosis, study and therapy of chronic inflammatory joint
XX PT and other diseases, comprises any of many specified genes or derived
XX PT proteins.
XX
XX Claim 1; Page; 12pp; German.
XX
XX This invention describes a novel reagent for diagnosis, molecular
XX CC definition and therapy of chronic inflammatory joint diseases, and other
XX CC inflammatory disorders, infective or tumour diseases in humans. The
XX CC products of the invention have antiinflammatory, cytostatic,
XX CC antiarthritic, antirheumatic and immunosuppressive activity and can be
XX CC used for gene therapy. The reagent of the invention and any proteins and
XX CC antibodies derived from it, are used (i) for analysing tissue and blood
XX CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
XX CC chronic joint diseases, on the basis of molecular characterisation, and
XX CC determining the etiological pathogenicity principle of as yet
XX CC uncharacterised inflammatory diseases, also monitoring progression and/or
XX CC treatment of disease, and optimisation of therapy and (iii) for
XX CC developing treatments for inflammatory diseases, particularly of joints,
XX CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides
XX CC used in the method of the invention
XX
XX Sequence 2492 BP; 553 A; 683 C; 790 G; 466 T; 0 U; 0 Other;
XX
XX Query Match 13.2%; Score 329; DB 8; Length 2492;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-148;
XX Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 187 GGCAGAGCCTCCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGGCCCCACG 246
XX DB 205 GGCAGAGCCTCCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGGCCCCACG 264
XX
XX 247 GGAGCTCGCGTGGGATCGACCTGGCCACCAACGAGGCGCAACCGACCCAGCTACGTGGC 366
XX DB 265 GGAGCTCGCGTGGGATCGACCTGGCCACCAACGAGGCGCAACCGACCCAGCTACGTGGC 394
XX
XX 307 GGCGCCGCTGGAGATCTTGCCCAACGACAGGCGCAACCGACCCAGCTACGTGGC 366
XX DB 325 GGCGCCGCTGGAGATCTTGCCCAACGACAGGCGCAACCGACCCAGCTACGTGGC 394
XX
XX 367 CTTACCCGACACCGAGCGGTGTGCGGGACGCGGCCAAGAGCCAGCGGCCCTGAACCC 426
XX DB 385 CTTACCCGACACCGAGCGGTGTGCGGGACGCGGCCAAGAGCCAGCGGCCCTGAACCC 444
XX
XX 427 CCACACACCGTTCGATGTCGCAAGCGGTGTGCGGGACGCGGCCAAGAGCCAGCGGT 486
XX DB 445 CCACACACCGTTCGATGTCGCAAGCGGTGTGCGGGACGCGGCCAAGAGCCAGCGGT 504
XX
XX 487 GCAGTCGACATGAAGCACTGGCCCTTCC 515
XX DB 505 GCAGTCGACATGAAGCACTGGCCCTTCC 533
XX
XX RESULT 12
XX ID AEF92617 standard; DNA; 2492 BP.
XX AC AEF92617;
XX XX
XX 20-APR-2006 (first entry)
XX
XX Human heat shock-related protein HS76, DNA.
XX
XX Diagnosis; ds; gene; neurodegenerative disease; Alzheimers disease;
XX KW dementia; cognitive disorder; Parkinsons disease; microarray;

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KW neuroprotective; nootropic; antiparkinsonian; screening; prognosis.
XX Homo sapiens.
XX WO2006020269-A2.
XX 23-FEB-2006.
XX
XX 19-JUL-2005; 2005WO-US025491.
XX 19-JUL-2004; 2004US-0589318P.
XX (UVRP ) UNIV ROCHESTER.
XX
XX Coleman PD, Federoff HJ, Maguire-Zeiss K, Myhre TR, Kurlan RM,
XX Cox C, Marshall F;
XX WPI; 2006-184393/19.
XX
XX Use of biomarkers for neurodegenerative disease for, e.g. diagnosing
XX PT neurodegenerative disease, screening therapeutic agent for treating
XX PT neurodegenerative disease, or monitoring neurodegenerative disease
XX PT progression.
XX
XX Example 1; SEQ ID NO 44; 552pp; English.
XX
XX The invention relates to using a biomarker for a neurodegenerative
XX CC disease for diagnosing a neurodegenerative disease, screening a
XX CC therapeutic agent for treating a neurodegenerative disease, monitoring a
XX CC neurodegenerative disease progression, monitoring a response to a
XX CC neurodegenerative disease treatment, identifying a risk for a
XX CC neurodegenerative disease, and differentially diagnosing a
XX CC neurodegenerative disease in a test subject. Also included are diagnosing
XX CC a neurodegenerative disease in a subject, screening for a therapeutic
XX CC agent for the treatment of a neurodegenerative disease, monitoring a
XX CC neurodegenerative disease progression in a subject, monitoring a response
XX CC to a neurodegenerative disease treatment in a subject, identifying a risk
XX CC for a neurodegenerative disease in a test subject, differentially
XX CC diagnosing a neurodegenerative disease in a test subject, a solid support
XX CC comprising one or more biomarkers, where the biomarker is one or more
XX CC proteins comprising HSP60, Dihydropyrimidine dehydrogenase, ER-60
XX CC protease, Glucose-6-phosphate dehydrogenase, ATP-synthase beta chain,
XX CC Annexin I, 14-3-3 epsilon, Prohibitin, Phosphoglycerate mutase 1,
XX CC Apolipoprotein AI, Superoxide dismutase, RNA-binding protein regulatory
XX CC subunit, Chain A thioredoxin peroxidase, B, RAS-related protein RAP1B,
XX CC and a solid support comprising one or more biomarkers (where the
XX CC tumor rejection antigen, Haptoglobin, Fibrin beta, or its combinations)
XX CC cyclin G1, weel, hTR2, CDC25b, GSK3 beta, protein kinase C alpha, C5, C1
XX CC inhibitor, IL-17r, IL-8, LIF, TNF-alpha, IL-10r, Alpha-1
XX CC antichymotrypsin, HSP 27, HSP 90, crystalline, GAPDH, ferritin H,
XX CC ferritin L, cox 1, cox 2, transferrin, or its combinations). The
XX CC biomarkers for the neurodegenerative disease are useful for diagnosing a
XX CC neurodegenerative disease, screening a therapeutic agent for treating a
XX CC neurodegenerative disease, monitoring a neurodegenerative disease
XX CC progression monitoring a response to a neurodegenerative disease
XX CC treatment, identifying a risk for a neurodegenerative disease, and
XX CC differentially diagnosing a neurodegenerative disease, e.g. Alzheimer's
XX CC disease and Parkinson's disease, in a test subject. The present sequence
XX CC is a DNA for a human biomarker, used in a microarray in the method of the
XX CC invention. NOTE: The specification describes AEF92574-AEF92813 (table 4)
XX CC as cDNA sequences yet some are protein sequences and some genomic DNA.
XX
XX Sequence 2492 BP; 553 A; 683 C; 790 G; 466 T; 0 U; 0 Other;
XX
XX Query Match 13.2%; Score 329; DB 15; Length 2492;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-148;
XX Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 187 GGCAGAGCCTCCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGGCCCCACG 246
XX DB 205 GGCAGAGCCTCCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGGCCCCACG 264

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QY 247 GGAGCTCGCGTGGGCATCGACCTGGGCAACCACTACTCTGCTGCGTGGCGGTGTTTCAGCA 306
D5 265 GGAGCTCGCGTGGGCATCGACCTGGGCAACCACTACTCTGCTGCGTGGCGGTGTTTCAGCA 324
QY 307 GGGCCGCTGGAGATCTCTGGCCAAACGACAGGGCAACCGCACCACTAGCTAGCTGGC 366
D5 325 GGGCCGCTGGAGATCTCTGGCCAAACGACAGGGCAACCGCACCACTAGCTAGCTGGC 384
QY 367 CTTACCGACACCGAGCGGCTGTCGGGGAACCGGCCAAGAGCCAGCGGCGCTTGAACCC 426
D5 385 CTTACCGACACCGAGCGGCTGTCGGGGAACCGGCCAAGAGCCAGCGGCGCTTGAACCC 444
QY 427 CCACAACCGCTGTCGATGTCGACGCGCTGATCGGGCGCAAGTTTCGGGACACACAGGT 486
D5 445 CCACAACCGCTGTCGATGTCGACGCGCTGATCGGGCGCAAGTTTCGGGACACACAGGT 504
QY 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
D5 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 13

ABA96361
ID ABA96361 standard; DNA; 1932 BP.

AC ABA96361;

DT 21-MAR-2002 (first entry)

DE Human schizophrenia/SCZ associated gene HSP70B SEQ ID NO 1.

XX Human; chromosome 1q22; SCZ; schizophrenia; in utero screening;
KW gene therapy; heat shock protein 70B; HSP70B; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..1932
FT /tag= a
FT /product= "SCZ/HSP70B"

XX WO200190412-A1.

XX 29-NOV-2001.

XX 23-APR-2001; 2001WO-US013086.

XX 21-APR-2000; 2000US-0198900P.

XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Brzustowicz LM, Bassett AS;

XX WPI; 2002-083121/11.

XX P-PSDB; ABA48711.

XX Diagnosing susceptibility to schizophrenia comprises determining presence
PT of allele of linked polymorphic marker on chromosome 1q22 and linked to
PT variant form of SCZ gene associated with schizophrenia phenotype.

XX Claim 19; Page 69-70; 83pp; English.

XX The invention relates to diagnosing susceptibility to schizophrenia in a
CC patient comprising determining the presence/absence of an allele of a
CC polymorphic marker in the DNA of a patient, where the polymorphic marker
CC is within the chromosome segment 1q22 bordered by D1S2705, D1S1679 and
CC linked to the DNA segment SCZ having a variant form associated with
CC phenotype of schizophrenia, where the allele is in phase with the variant
CC form of SCZ and the presence of the allele indicates susceptibility to
CC schizophrenia. The method can be used for in utero screening of fetuses
CC for the presence of a variant SCZ allele. Identification of such
CC variations offers the possibility of gene therapy and for couples known
CC to be at risk of giving rise to an affected progeny, diagnosis can be

CC combined with in vitro reproduction procedures to identify an embryo
CC having wild-type SCZ alleles before implantation. Screening children
CC shortly after birth allows administration of appropriate treatment at an
CC early stage of detection. The genetic tests provide a highly accurate
CC assay for diagnosing schizophrenia and schizophrenia susceptibility. The
CC SCZ gene encodes a previously isolated sequence encoding human heat shock
CC protein 70B (HSP70B, GenBank Accession Number NM002155)

XX Sequence 1932 BP; 423 A; 552 C; 632 G; 325 T; 0 U; 0 Other;

Query Match 11.4%; Score 283; DB 6; Length 1932;
Best Local Similarity 100.0%; Pred. No. 2.3e-126;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 ATGCAGGCCCCACGGGAGCTCGCGTGGGATCGACCTGGGCACCACTACTCTGCGTG 292
D5 1 ATGCAGGCCCCACGGGAGCTCGCGTGGGATCGACCTGGGCACCACTACTCTGCGTG 60

QY 293 GCGCTGTTTCAGCAGGGCCGCGTGGGATCTCTGCCAACACCAAGGGCAACCCACACG 352
D5 61 GCGCTGTTTCAGCAGGGCCGCGTGGGATCTCTGCCAACACCAAGGGCAACCCACACG 120

QY 353 CCCAGCTACGTGGCTTTCACCGACACCGAGCGGTGGTGGGGACCGGCCAAGGCCAG 412
D5 121 CCCAGCTACGTGGCTTTCACCGACACCGAGCGGTGGTGGGGACCGGCCAAGGCCAG 180

QY 413 GCGGCCCTGAACCCCCCAACACCGCTGTTGATGCCAAGCGGTGATCGGGCGCAAGTTC 472
D5 181 GCGGCCCTGAACCCCCCAACACCGCTGTTGATGCCAAGCGGTGATCGGGCGCAAGTTC 240

QY 473 GCGGACACCAACCGTGCAGTCGACATGAACACTGGCCCTTCC 515

D5 241 GCGGACACCAACCGTGCAGTCGACATGAACACTGGCCCTTCC 283

RESULT 14

ID ADD18651 standard; DNA; 1932 BP.

AC ADD18651;

DT 15-JAN-2004 (first entry)

DE Human disease related protein DNA sequence SeqID82.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing; gene; ds.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX P-PSDB; ADD18650.

XX New substantially purified polypeptide, useful for diagnosing or treating

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Result No.	Score	Query			Description		
		Match	Length	ID	ID	ID	ID
1	484	19.4	2336	3	US-09-919-039-203	Sequence 203, Appli	
2	431	17.3	2962	3	US-09-566-921-72	Sequence 72, Appli	
3	329	13.2	2379	3	US-08-797-358B-2	Sequence 2, Appli	
4	120	4.8	968	3	US-09-023-655-1112	Sequence 1112, Ap	
5	100	4.0	222	3	US-09-376-774-3	Sequence 3, Appli	
6	100	4.0	469	3	US-09-185-243-1	Sequence 1, Appli	
7	100	4.0	550	3	US-09-398-522-111	Sequence 111, Appli	
8	100	4.0	10728	3	US-09-376-774-5	Sequence 5, Appli	
9	85	3.4	159	3	US-09-513-999C-14057	Sequence 14057, A	
10	71	2.8	2394	3	US-08-797-358B-1	Sequence 1, Appli	
11	58	2.3	119	5	US-09-936-506-3	Sequence 3, Appli	
12	50	2.0	50	3	US-10-131-827-2355	Sequence 2255, Ap	
13	50	2.0	50	5	US-10-131-831-2355	Sequence 2255, Ap	
14	45	1.8	45	1	US-08-171-389-185	Sequence 185, App	
15	45	1.8	45	2	US-08-123-936-185	Sequence 185, App	
16	45	1.8	45	2	US-08-475-228A-185	Sequence 185, App	
17	45	1.8	45	3	US-08-482-080A-185	Sequence 185, App	
18	45	1.8	45	3	US-09-354-947-185	Sequence 185, App	
19	45	1.8	45	3	US-09-593-346-185	Sequence 185, App	
20	45	1.8	45	7	PCT-US93-12388-185	Sequence 185, App	
21	42	1.7	53	2	US-08-171-389-186	Sequence 186, App	
22	42	1.7	53	2	US-08-123-936-186	Sequence 186, App	
23	42	1.7	53	2	US-08-475-228A-186	Sequence 186, App	

Qy 452 CGGCTGATCGGGCGCAAGTTCCGCGACACCAACGCTGAGTCGAGCATGAAGCATCTGGCCC 511
Db 329 CGGCTGATCGGGCGCAAGTTCCGCGACACCAACGCTGAGTCGAGCATGAAGCATCTGGCCC 388
Qy 512 TTCCAGGTGGTGAGCGGGCGCAAGCCCAAGGTGCGCGTATGCTACCGCGGGAGGAC 571
Db 389 TTCCGGGTGGTGAGCGGGCGCAAGCCCAAGGTGCGCGTATGCTACCGCGGGAGGAC 448
Qy 572 AAGAGCTTTCTACCCGAGGAGATCTCGTCCATGTGTGCTGAGCAAGATGAAGAGACGGCC 631
Db 449 AAGAGCTTTCTACCCGAGGAGATCTCGTCCATGTGTGCTGAGCAAGATGAAGAGACGGCC 508
Qy 632 GAGGCTACCTGGGCGACCCGCTGAAGACACGAGTGATCACGTCGCCCACTATTTCAGT 691
Db 509 GAGGCTACCTGGGCGACCCGCTGAAGACACGAGTGATCACGTCGCCCACTATTTCAGT 568
Qy 692 AACTCGAGCGCCAGGCGCACCAAGGACGCGGGGCCATCGCGGGGCTCAAGGTGCTGCCG 751
Db 569 GACTCGAGCGCCAGGCGCACCAAGGACGCGGGGCCATCGCGGGGCTCAAGGTGCTGCCG 628
Qy 752 ATCATCAATGAGGCCACGCGAGCCATCGCTATGGGCTGGACCGCGGGCGCGGGA 811
Db 629 ATCATCAATGAGGCCACGCGAGCTGCCATCGCTATGGGCTGGACCGCGGGCGCGGGA 688
Qy 812 AAGCGCAACGTGCTCAATTTTGAACCTGGGTGGGGCACCTTCGATGTGTGCGTCTCTCC 871
Db 689 GAGCGCAACGTGCTCAATTTTGAACCTGGGTGGGGCACCTTCGATGTGTGCGTCTCTCC 748
Qy 872 ATTGACGCGGTGCTTTGAGGTGAAGCCACTGCTGAGATACCCACTCGGAGGAGAG 931
Db 749 ATTGACGCGGTGCTTTGAGGTGAAGCCACTGCTGAGATACCCACTCGGAGGAGAG 808
Qy 932 GACTTCGACAACCGGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 991
Db 809 GACTTCGACAACCGGCTCGTGAACCACTTCATGGAAGAAATTCGCGCGGAACATGGGAAG 868
Qy 992 GACTGAGCGGGAAACAAGGTGCCCTGCGAGGCTGCGCACAGCTGTGAGCGGCCAAG 1051
Db 869 GACTGAGCGGGAAACAAGGTGCCCTGCGAGGCTGCGCACAGCTGTGAGCGGCCAAG 928
Qy 1052 CGCACCCGCTCTCCAGACACCGAGCCACCTGGAGATAGACTCCCTGTCGAGGGGTG 1111
Db 929 CGCACCCGCTCTCCAGACACCGAGCCACCTGGAGATAGACTCCCTGTCGAGGGGTG 988
Qy 1112 GACTTCTACAAGTCCATCACTGTCGCGCTTTTGAAGAACTGTGCTCAGACCTCTTCCGC 1171
Db 989 GACTTCTACAAGTCCATCACTGTCGCGCTTTTGAAGAACTGTGCTCAGACCTCTTCCGC 1048
Qy 1172 AGCACCTTGAGCCGGTGAGAGCCCTTGGGATGCGCAAGCTGGACAGGCCCAAGATT 1231
Db 1049 AGCACCTTGAGCCGGTGAGAGCCCTTGGGATGCGCAAGCTGGACAGGCCCAAGATT 1108
Qy 1232 CATGACTTCTGCTCGGGGGGGGCTCCACTCGCATCCCAAGGTGCAAGAGTTGCTGCA 1291
Db 1109 CATGAGCTGCTCTGCTGGG- GGGGCTCCACAGCATCCCAAGGTGCAAGAGTTGCTGCA 1167
Qy 1292 GGAATCTTCAACGCAAGGAGCTGAACAAGAGCTCAACCTGATGAGGCTGTGGCCTA 1351
Db 1168 GGAATCTTCAACGCAAGGAGCTGAACAAGAGCTCAACCTGATGAGGCTGTGGCCTA 1227
Qy 1352 TGGGCTGCTGTGTCAGGCGCGCGTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT 1411
Db 1228 TGGGCTGCTGTGTCAGGCGCGCGTGTGATGGGGGACAAATGTGAGAAAGTGCAGGATCT 1287
Qy 1412 CCGTGTGCTGATGAGTGGCTCCCTGCTCTGCGGCTGGAGACAGCAGGTGGGTGATGAC 1471
Db 1288 CCGTGTGCTGATGAGTGGCTCCCTGCTCTGCGGCTGGAGACAGCAGGTGGGTGATGAC 1347
Qy 1472 CACGCTGATCCAGAGGAACGCCACTATCCCAACCAAGCAGACCCAGACTTTTCAACACCTA 1531
Db 1348 CACGCTGATCCAGAGGAACGCCACTATCCCAACCAAGCAGACCCAGACTTTTCAACACCTA 1407

Qy 1532 CTCGGACAACAGCCTGGGCTCTTCATCCAGGTGTATGAG 1572
Db 1408 CTCGGACAACAGCCTGGGCTCTTCATCCAGGTGTATGAG 1448

RESULT 2

US-09-566-921-72
; Sequence 72, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 72
; LENGTH: 2962
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 349676.8
US-09-566-921-72

Query Match 17.3%; Score 431; DB 3; Length 2962;

Best Local Similarity 99.8%; Pred. No. 2e-202;

Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CCGTGGCTTCAGCATCCGACAAGATTCAGCCATGCGAGGCCCAACGGAGCTCGCG 257
Db 699 CCGTGGCTTCAGCATCCGACAAGATTCAGCCATGCGAGGCCCAACGGAGCTCGCG 758
Qy 258 TGGGCATCGACCTGGGCGACCACTACTCGTGGTGGCGCTGTTTACGAGGGCGCGTGG 317
Db 759 TGGGCATCGACCTGGGCGACCACTACTCGTGGTGGCGCTGTTTACGAGGGCGCGTGG 818
Qy 318 AGATCTCTGGCCCAACGACAGCGCAACCGCACCGCCAGCTACGTGGCCCTTACCCGACA 377
Db 819 AGATCTCTGGCCCAACGACAGCGCAACCGCACCGCCAGCTACGTGGCCCTTACCCGACA 878
Qy 378 CCGAGCGGCTGGTGGGAGCGCGCCCAAGAGCGCAGGGGCCCTTGAACCCCAACACCG 437
Db 879 CCGAGCGGCTGGTGGGAGCGCGCCCAAGAGCGCAGGGGCCCTTGAACCCCAACACCG 938
Qy 438 TGTTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACCAACGAGTCGAGTCGGA 497
Db 939 TGTTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACCAACGAGTCGAGTCGGA 998
Qy 498 TGAAGCATGTCGCCCTTCCAGTGGTGAGCGAGGGCGCAAGCCCAAGGTGCGCGTATGCT 557
Db 999 TGAAGCATGTCGCCCTTCCAGTGGTGAGCGAGGGCGCAAGCCCAAGGTGCGCGTATGCT 1058
Qy 558 ACCCGGGGAGGACAAGACGTTCTACCCCGAGGAGATCTCGTCATGGTGTGAGCAGA 617
Db 1059 ACCCGGGGAGGACAAGACGTTCTACCCCGAGGAGATCTCGTCATGGTGTGAGCAGA 1118
Qy 618 TGAAGGAGACGGCGAGCGGTACCTGGGCGCAGCCGTCGAGCAGCAGTATCACCGTGC 677
Db 1119 TGAAGGAGACGGCGAGCGGTACCTGGGCGCAGCCGTCGAGCAGCAGTATCACCGTGC 1178
Qy 678 CC 679
Db 1179 CC 1180

RESULT 3

US-08-797-358B-2
; Sequence 2, Application US/08797358B
; Patent No. 6268478

GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2379 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-797-358B-2

Query Match 13.2%; Score 329; DB 3; Length 2379;
Best Local Similarity 100.0%; Pred. No. 5.1e-152;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 GGCAGCAGCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATCAGGCCCGCCAG 246
Db 205 GGCAGCAGCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATCAGGCCCGCCAG 264
QY 247 GGAGCTCGGCTGGGATCGACTGGGCAACCTACTACTCTGCTGGGGCTGTTTCAGCA 306
Db 265 GGAGCTCGGCTGGGATCGACTGGGCAACCTACTACTCTGCTGGGGCTGTTTCAGCA 324
QY 307 GGGCCGCTGGAGATCTCGGCAACAGCAGGGCAACCGCACCGCCAGCTAGTGGC 366
Db 325 GGGCCGCTGGAGATCTCGGCAACAGCAGGGCAACCGCACCGCCAGCTAGTGGC 384
QY 367 TTTCACCGACACCGAGCGCTGCTGGGCAACAGCAGGGCAACCGCACCGCCAGCTAGTGGC 426
Db 385 TTTCACCGACACCGAGCGCTGCTGGGCAACAGCAGGGCAACCGCACCGCCAGCTAGTGGC 444
QY 427 CCACAAACCGTGTTCGATGCGAAGCGGCTGATCGGGCGCAAGTTGCGGACACCAACGAT 486
Db 445 CCACAAACCGTGTTCGATGCGAAGCGGCTGATCGGGCGCAAGTTGCGGACACCAACGAT 504
QY 487 GCAGTCGGACATGAAGCACTGGCCCTTC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTC 533

RESULT 4
US-09-023-655-1112
; Sequence 1112, Application US/09023655
; Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1112:
SEQUENCE CHARACTERISTICS:
LENGTH: 968 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g184413
US-09-023-655-1112
Query Match 4.8%; Score 120; DB 3; Length 968;
Best Local Similarity 98.9%; Pred. No. 9.6e-49;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 530 GCGCGCAAGCCCAAGTGGCTATGCTACCGGGGAGGACAAAGCTTCTACCCCGAG 589
Db 525 GCGCGCAAGCCCAAGTGGCTATGCTACCGGGGAGGACAAAGCTTCTACCCCGAG 584
QY 590 GAGATCTCGTCCATGCTGAGCAAGATGAAGAGAGCGCGGAGCGGTACTGGGCCAG 649
Db 585 GAGATCTCGTCCATGCTGAGCAAGATGAAGAGAGCGCGGAGCGGTACTGGGCCAG 644
QY 650 CCGGTGAAGCAGCAGTGTATCACCGTGGCCACCTATTTTCAGTAACTCGCAGCGCCAGCC 709
Db 645 CCGGTGAAGCAGCAGTGTATCACCGTGGCCACCTATTTTCAGTAACTCGCAGCGCCAGCC 704
QY 710 ACCAAGACGCGGGGCCCATCGCGGGCTCAAGGTGCTGCGGATCATCAATGAGGCCAG 769
Db 705 ACCAAGACGCGGGGCCCATCGCGGGCTCAAGGTGCTGCGGATCATCAATGAGGCCAG 764
QY 770 GCAGCAGCCATCGCCTATGGGCTGGACCGCGG 802
Db 765 GCAGCAGCCATCGCCTATGGGCTGGACCGCGG 797

RESULT 5
US-09-376-774-3
; Sequence 3, Application US/09376774

; Patent No. 6759236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Gomer, Charles
; APPLICANT: T'Ang, Anne
; TITLE OF INVENTION: Methods To Enhance And Confine Expression
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT APPLICATION NUMBER: US/09/376,774
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 3
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: gene
; OTHER INFORMATION: heat shock response element of human heat shock 70
; OTHER INFORMATION: Gene promoter
US-09-376-774-3

Query Match 4.0%; Score 100; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 7e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 60
Db 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 60

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100

RESULT 5

US-09-185-243-1
; Sequence 1, Application US/09185243
; Patent No. 6709858
; GENERAL INFORMATION:
; APPLICANT: Tsang, Tom
; APPLICANT: Gerner, Eugene W.
; APPLICANT: Harris, David T.
; APPLICANT: Hersh, Evan
; TITLE OF INVENTION: Hyperthermic Inducible Expression Vectors for Gene
; TITLE OF INVENTION: Therapy and Methods of Use Thereof
; FILE REFERENCE: 15907-0016
; CURRENT APPLICATION NUMBER: US/09/185,243
; CURRENT FILING DATE: 1998-11-03
; EARLIER APPLICATION NUMBER: US 60/064,088
; EARLIER FILING DATE: 1997-11-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-185-243-1

Query Match 4.0%; Score 100; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 60
Db 246 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 305

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 306 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 345

RESULT 7

US-09-398-522-111
; Sequence 111, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (0)...(0)
; OTHER INFORMATION: HSPA6 CpG Island
US-09-398-522-111

Query Match 4.0%; Score 100; DB 3; Length 550;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 60
Db 336 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 395

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 396 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 435

RESULT 8

US-09-376-774-5
; Sequence 5, Application US/09376774
; Patent No. 6759236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Gomer, Charles
; APPLICANT: T'Ang, Anne
; TITLE OF INVENTION: Methods To Enhance And Confine Expression
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT APPLICATION NUMBER: US/09/376,774
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 10728
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: recombinant vector pDATH-TNF?
US-09-376-774-5

Query Match 4.0%; Score 100; DB 3; Length 10728;
Best Local Similarity 100.0%; Pred. No. 8e-39;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 60
Db 6 CCCGGCGGGCGGGCGGAGGCTCTCGACTGGCGGGGAAGTGCGGGAAGTTCCCGGCG 65

Qy 61 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 100
Db 66 GCGGGTTCGGGAGGTGCAAAAGGATGAAAAGCCCGTGA 105

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RESULT 9
US-09-513-999C-14057
; Sequence 14057, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14057
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 71
; OTHER INFORMATION: s=g or c
US-09-513-999C-14057

Query Match 3.4%; Score 85; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.8e-31;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GGCAGCAGCCTCGTGGCTTCCAGCATCCGACACAGAGCTTCAGCCATGCGGCCCCACG 246
Db 72 GGCAGCAGCCTCGTGGCTTCCAGCATCCGACACAGAGCTTCAGCCATGCGGCCCCACG 131

QY 247 GAGCTCGCGTGGCATCGACCTG 271
Db 132 GGAGCTCGCGTGGCATCGACCTG 156

RESULT 10
US-08-797-358B-1
; Sequence 1, Application US/08797358B
; Patent No. 6268478
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 11-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CE 3165
; TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-797-358B-1

Query Match 2.8%; Score 71; DB 3; Length 2394;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1491 GCCACTATCCCAACCAAGCAGACCCAGACTTTCCACCTACTCTCGGACACCGCTGGG 1550
Db 1512 GCCACTATCCCAACCAAGCAGACCCAGACTTTCCACCTACTCTCGGACACCGCTGGG 1571

QY 1551 GTCTTCATCCA 1561
Db 1572 GTCTTCATCCA 1582

RESULT 11
US-09-936-506-3
; Sequence 3, Application US/09936506
; Patent No. 7034142
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; APPLICANT: Coste, Herve J-C
; APPLICANT: Ellis, Jonathan H
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PF3623/WO
; CURRENT APPLICATION NUMBER: US/09/936,506
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: GB 9905498.3
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-936-506-3

Query Match 2.3%; Score 58; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.9e-18;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GCGGGCTGGCGGCGAGAGAAACCGCAGGAGAGCCTCACTGCTAGCGCCCTCGACG 179
Db 11 GCGGGCTGGCGGCGAGAGAAACCGCAGGAGAGCCTCACTGCTAGCGCCCTCGACG 68

RESULT 12
US-10-131-827-2255
; Sequence 2255, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN-
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
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; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2255
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2255

Query Match      2.0%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1991 GGCAGAGAGGAGGAGTATGACATCAGAGAGGAGGAGCTGGAGCAAAATCT 2040
Db 1 GGCAGAGAGGAGGAGTATGACATCAGAGAGGAGGAGCTGGAGCAAAATCT 50

RESULT 13
US-10-131-831-2255
; Sequence 2255, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2255
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-2255

Query Match      2.0%; Score 50; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1991 GGCAGAGAGGAGGAGTATGACATCAGAGAGGAGGAGCTGGAGCAAAATCT 2040
Db 1 GGCAGAGAGGAGGAGTATGACATCAGAGAGGAGGAGCTGGAGCAAAATCT 50

RESULT 14
US-08-171-389-185
; Sequence 185, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human hsp70B gene
US-08-171-389-185

Query Match      1.8%; Score 45; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGCGGGCGGAGGCTCTCGACTGGCGGGAGGAGCTGGCGGAGGCT 52
Db 1 GGGCGGGCGGAGGCTCTCGACTGGCGGGAGGAGCTGGCGGAGGCT 45

RESULT 15
US-08-123-936-185
; Sequence 185, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,936
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human hsp70B gene
;
US-08-123-936-185

Query Match      1.8%; Score 45; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GGCGGGCGGGAGGCTCTGACTGGCGGGAGGTCGGGAGGT 52
Db      1 GGCGGGCGGGAGGCTCTGACTGGCGGGAGGTCGGGAGGT 45

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GenCore version 5.1.9
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(without alignments)
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Perfect score: 2493
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Gapop 60.0 , Gapext 60.0
Searched: 18892170 seqs, 6143817638 residues
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Total number of hits satisfying chosen parameters: 37781012
Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published Applications NA Main.*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	19.9	2361	3	US-09-925-302-281
2	495	19.9	2361	3	US-09-925-302-281
3	484	19.4	2336	6	US-09-919-039-203
4	431	17.3	2962	6	US-10-002-600-97
5	431	17.3	2962	10	US-10-765-700-72
6	429	17.2	531	8	US-10-637-855-217
7	329	13.2	2492	3	US-09-968-007A-527
8	329	13.2	2492	9	US-10-278-698-290
9	329	13.2	2492	9	US-10-278-698-804
10	329	13.2	2492	10	US-10-843-641A-6997
11	283	11.4	1932	8	US-10-755-889-395
12	260	10.4	819	6	US-10-027-632-170807
13	260	10.4	819	7	US-10-027-632-170807
14	259	10.4	397	4	US-09-925-065A-12443
15	259	10.4	397	5	US-09-925-065A-12443
16	259	10.4	397	12	US-10-301-480-113680
17	259	10.4	397	12	US-10-301-480-727089

C 18	253	10.1	777	6	US-10-027-632-168525	Sequence 168525,
C 19	253	10.1	777	6	US-10-027-632-168526	Sequence 168526,
C 20	253	10.1	777	7	US-10-027-632-168525	Sequence 168525,
C 21	253	10.1	777	7	US-10-027-632-168526	Sequence 168526,
22	120	4.8	968	8	US-10-641-643-1112	Sequence 1112, Ap
23	104	4.2	276	9	US-10-425-115-87729	Sequence 87729, A
24	100	4.0	286	6	US-10-096-549-4	Sequence 4, Appli
25	100	4.0	286	10	US-10-864-102-4	Sequence 4, Appli
26	100	4.0	469	7	US-10-152-577-1	Sequence 1, Appli
27	100	4.0	469	10	US-10-108-486-1	Sequence 1, Appli
28	100	4.0	469	11	US-10-733-280-1	Sequence 1, Appli
29	100	4.0	550	9	US-10-930-301-111	Sequence 111, App
30	100	4.0	592	6	US-10-172-399-13	Sequence 13, Appl
31	100	4.0	592	10	US-10-501-756-22	Sequence 22, Appl
32	100	4.0	714	9	US-10-489-136-27	Sequence 27, Appl
C 33	99	4.0	370	4	US-09-925-065A-561882	Sequence 561882,
C 34	99	4.0	370	5	US-09-925-065A-561882	Sequence 561882,
35	79	3.2	268	9	US-10-425-115-1630	Sequence 1630, Ap
36	76	3.0	475	3	US-09-918-995-31483	Sequence 31483, A
37	60	2.4	60	3	US-09-908-975-11556	Sequence 11556, A
38	58	2.3	119	15	US-11-167-614-3	Sequence 3, Appli
39	50	2.0	50	7	US-10-131-827-2255	Sequence 2255, Ap
40	48	1.9	768	9	US-10-363-345A-20773	Sequence 20773, A
41	48	1.9	768	9	US-10-363-345A-20774	Sequence 20774, A
42	48	1.9	768	10	US-10-363-483A-20773	Sequence 20773, A
C 43	48	1.9	768	10	US-10-363-483A-20774	Sequence 20774, A
44	45	1.8	45	3	US-09-993-346-185	Sequence 185, App
45	42	1.7	53	3	US-09-993-346-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-09-925-302-281
; Sequence 281, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2352)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2355)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-281

Query Match 19.9%; Score 495; DB 3; Length 2361;
Best Local Similarity 99.8%; Pred. No. 4.6e-250;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 134 GCAGAGAACCCGAGGAGAGCCCTCACTGCTAGGCGCCCTCGAGCGGCGGAGCGGAGCA 193
DB 72 GCAGAGAACCCGAGGAGAGCCCTCACTGCTAGGCGCCCTCGAGCGGCGGAGCGGAGCA 131

194 GCCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGAGCCCGCCAGCGAGCTC 253
 132 GCCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGAGCCCGCCAGCGAGCTC 191
 254 GCCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGAGCCCGCCAGCGAGCTC 313
 192 GCCTCGTGGCTCCAGCATCCGACAAAGCTTCAGCCATGCGAGCCCGCCAGCGAGCTC 251
 314 GTGGAGATCTCGGCAACGACGAGGCAACCGCAACCGCCAGCTTACGTCGCTTCACC 373
 252 GTGGAGATCTCGGCAACGACGAGGCAACCGCAACCGCCAGCTTACGTCGCTTCACC 311
 374 GACACCGAGCGGCTGCTCGGGGACGCGGCCAAGAGCGAGCGCGCCCTGAACCCCCACAC 433
 312 GACACCGAGCGGCTGCTCGGGGACGCGGCCAAGAGCGAGCGCGCCCTGAACCCCCACAC 371
 434 ACCGTGTTGATGCGCAAGCGGCTGATCGGGCGCAAGTTTCGCGGACACCGTGCAGTCG 493
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 494 GACATGAAGCACTGGCCCTTCCAGGTTGAGCGAGCGCGGCCAAGCGGTCGCGCTA 553
 432 GACATGAAGCACTGGCCCTTCCAGGTTGAGCGAGCGCGGCCAAGCGGTCGCGCTA 491
 554 TGCTACCGCGGGAGGACAAAGCTTCTACCCCGAGGAGATCTCGTCCATGCTGAGC 613
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 614 AAGATGAAGGAGACGCGCGAGCGCTACCTGGGCGCAGCCCGTGAAGCAGCGATGATCACC 673
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 674 GTGCCC 679
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RESULT 2
 US-09-925-302-281
 ; Sequence 281, Application US/09925302
 ; Publication No. US20030084072A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA104
 ; CURRENT APPLICATION NUMBER: US/09/925,302
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05918
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 896
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 281
 ; LENGTH: 2361
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (45)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2352)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2355)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-925-302-281
 Query Match 19.9%; Score 495; DB 3; Length 2361;
 Best Local Similarity 99.8%; Pred. No. 4.6e-250;
 Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

134 GCAGAGAAACCGAGGAGAGGCTTCACTGCTAGCGCCCTCGAGCGGCGAGCGGAGCA 193
 72 GCAGAGAAACCGAGGAGAGGCTTCACTGCTAGCGCCCTCGAGCGGCGAGCGGAGCA 131
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 372 ACCGTGTTGATGCGCAAGCGGCTGATCGGGCGCAAGTTTCGCGGACACCGTGCAGTCG 431
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 432 GACATGAAGCACTGGCCCTTCCAGGTTGAGCGAGCGCGGCCAAGCGGTCGCGCTA 491
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 614 AAGATGAAGGAGACGCGCGAGCGCTACCTGGGCGCAGCCCGTGAAGCAGCGATGATCACC 673
 552 AAGATGAAGGAGACGCGCGAGCGCTACCTGGGCGCAGCCCGTGAAGCAGCGATGATCACC 611
 674 GTGCCC 679
 612 GTGCCC 617

RESULT 3
 US-09-919-039-203
 ; Sequence 203, Application US/09919039
 ; Publication No. US20030108871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 203
 ; LENGTH: 2336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030108871A1 1440032CB1
 ; US-09-919-039-203

Query Match 19.4%; Score 484; DB 3; Length 2336;
 Best Local Similarity 98.8%; Pred. No. 3e-244;
 Matches 1404; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
 152 GAGCCTCACTGCTGAGCGCCCTCGACCGCGGAGCGGAGCGAGCTCGGTCGCTCCAGC 211
 29 GAGCCTCACTGCTGAGCGCCCTCGACCGCGGAGCGGAGCGAGCTCGGTCGCTCCAGC 88
 212 ATCCGACAAAGAGCTTCAGCCATGCGAGCGCCCGAGCGGAGCTCGCGGTGGGATCGACCTG 271

Db 89 ATCCGACAAAGAGCTTACGCCATCAGGCCCCACGGAGCTCGCGGTGGGCATCGACCTG 148
Qy 272 GGCAACCACTACTCTGCTGGGCGTGTTCAGCAGGCGCGCTGGAGATCTCTGGCCCAAC 331
Db 149 GGCACCACTACTCTGCTGGGCGTGTTCAGCAGGCGCGCTGGAGATCTCTGGCCCAAC 208
Qy 332 GACAGGGCAACCGGACCAAGCCCAAGTACGTGGCTCTTCCAGACACCGAGCGGCTGGTC 391
Db 209 GACAGGGCAACCGGACCAAGCCCAAGTACGTGGCTCTTCCAGACACCGAGCGGCTGGTC 268
Qy 392 GGGGACCGGCGCAAGAGCCAGGCGGCGCTGNAACCCCAACACACCGGTTCGATGCCAAG 451
Db 269 GGGGACCGGCGCAAGAGCCAGGCGGCGCTGNAACCCCAACACACCGGTTCGATGCCAAG 328
Qy 452 CGGCTGATCGGCGCGCAAGATTCGCGGACACCAAGGTGCGAGTCCGACATGAAGCACTGGCCC 511
Db 329 CGGCTGATCGGCGCGCAAGATTCGCGGACACCAAGGTGCGAGTCCGACATGAAGCACTGGCCC 388
Qy 512 TTCCAGGTGTGAGCGAGGCGGCAAGCCCAAGGTGCGCGTATGCTACCGCGGGAGGAC 571
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Db 449 AAGACGTTCTACCCGAGGAGATCTCTGTCATGCTGTGACCAAGATGAAGGAGCGGCC 508
Qy 632 GAGCGGTACCTGGGCGAGCGCGTGAAGCACGACGTGATCAAGTCCGCGCCACTATTTCAGT 691
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Qy 692 AACTCGCAGCGCCAGGCGCACCAAGGACGCGGGGCGCATCGCGGGGTCAAGGTGCTGCCG 751
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Qy 752 ATCATCAATGAGGCGACGCGACGACCATGCGCTATGCGGTGACACCGCGGGCGCGGGA 811
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Qy 812 AAGCGCAACGTGCTCATTTTACCTGGGTGGGGGACCTTCGATGTGCTGCTCTCC 871
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Qy 872 ATTGACCGCGGTGCTTTGAGGTGAAGCACTGCTGGAGATACCCACCTGGGAGGAGAG 931
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Qy 992 GACTGAGCGGGAACAAGCGTGCCTCGCAGAGCTGCGCACAGCCTGTGAGCGCGCCAAG 1051
Db 869 GACTGAGCGGGAACAAGCGTGCCTCGCAGAGCTGCGCACAGCCTGTGAGCGCGCCAAG 928
Qy 1052 CGCACCCCGCTCTCCAGCACCCAGGCCACCTCGAGATAGACTCCCTGTTTCGAGGGCGTG 1111
Db 929 CGCACCCCGCTCTCCAGCACCCAGGCCACCTCGAGATAGACTCCCTGTTTCGAGGGCGTG 988
Qy 1112 GACTTCTCAAGTCCATCACTGTCGCGCGCTTTGAGGAACTGTGCTCAGACCTCTTCCCG 1171
Db 989 GACTTCTCAAGTCCATCACTGTCGCGCGCTTTGAGGAACTGTGCTCAGACCTCTTCCCG 1048
Qy 1172 AGCACCTCGAGCGCGTGGAGAGGCGCTCGGGGATGSCCAAGCTGGACAGGCGCCAGATT 1231
Db 1049 AGCACCTCGAGCGCGTGGAGAGGCGCTCGGGGATGSCCAAGCTGGACAGGCGCCAGATT 1108
Qy 1232 CATGACTTCGTTCTGGGGGAGGCGCTCCACTCGCATCCCAAGGTGAGAAAGTTGCTGCA 1291
Db 1109 CATGAGTCTGTTCTGGTGGG-GGGCTCCACACGATCCCAAGGTGAGAAAGTTGCTGCA 1167
Qy 1292 GGACTTCTCAAGCGCAAGGAGCTGAACAAGAGCATCAACCTCGATGAGGCTGTGGCTTA 1351

Db 1168 GGAATTTCTTCAACGCGCAAGGAGCTGAACAAGAGCATCAACCTGTAGGCTGTGGCCTA 1227
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Qy 1412 CTTGCTGTGATGTGGCTCTCCCTGTCTCTGCGGCTGGAGACAGAGGTGGGCTGATGAC 1471
Db 1288 CTTGCTGTGATGTGGCTCTCCCTGTCTCTGCGGCTGGAGACAGAGGTGGGCTGATGAC 1347
Qy 1472 CAGCTGATCCAGAGGAAAGCGCACTATCCCAACCAAGCAGACCCAGCTTTCAACCACTA 1531
Db 1348 CAGCTGATCCAGAGGAAAGCGCACTATCCCAACCAAGCAGACCCAGCTTTCAACCACTA 1407
Qy 1532 CTGCGAACAACCGCTGGGCTTTTCATCCAGGTGTATGAGG 1572
Db 1408 CTGCGAACAACCGCTGGGCTTTTCATCCAGGTGTATGAGG 1448

RESULT 4
US-10-002-600-97
; Sequence 97, Application US/10002600
; Publication No. US20020137077A1
; GENERAL INFORMATION:
; APPLICANT: Hopkins, Christopher M.
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS
; FILE REFERENCE: PA-0042 US
; CURRENT APPLICATION NUMBER: US/10/002,600
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/243,521
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PERL Program
; SEQ ID NO 97
; LENGTH: 2962
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Template ID: 349676.8
US-10-002-600-97

Query Match 17.3%; Score 431; DB 6; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3e-216;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 198 CCGTGGCTTCCAGCATCCGACCAAGAGCTTCAAGCCATGAGGCCCGCCACCGGAGCTCGCG 257
Db 699 CCGTGGCTTCCAGCATCCGACCAAGAGCTTCAAGCCATGAGGCCCGCCACCGGAGCTCGCG 758
Qy 258 TGGGATTCAGCTGGGACCACTACTCTGCTGGGCGTGTTCAGAGGGCGCGTGG 317
Db 759 TGGGATTCAGCTGGGACCACTACTCTGCTGGGCGTGTTCAGAGGGCGCGTGG 818
Qy 318 AGATCTGCGCAACGACGAGGCAACCGCACACCGCCAGCTACGTGGCTTCCACGACA 377
Db 819 AGATCTGCGCAACGACGAGGCAACCGCACACCGCCAGCTACGTGGCTTCCACGACA 878
Qy 378 CCGAGCGGCTGTTCGGGAGCGCGCCCAAGAGCGCGGCGCCCTTGAACCCCAACACCG 437
Db 879 CCGAGCGGCTGTTCGGGAGCGCGCCCAAGAGCGCGGCGCCCTTGAACCCCAACACCG 938
Qy 438 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTCCGCGACCAACCGTGCAGTCCGACA 497
Db 939 TGTTCGATGCCAAGCGGCTGATCGGCGCAAGTTCCGCGACCAACCGTGCAGTCCGACA 998
Qy 498 TGAAGCACTGGCCCTTCCAGGTGCTGAGCGGCGGCAAGCCCAAGGTGCGGCTATGCT 557
Db 999 TGAAGCACTGGCCCTTCCAGGTGCTGAGCGGCGGCAAGCCCAAGGTGCGGCTATGCT 1058

QY 558 ACCCGGGGAGGACAGACGTTCTTACCCCGAGGAGATCTCTCCATGCTGTGAGCAAGA 617
Db 1059 ACCCGGGGAGGACAGACGTTCTTACCCCGAGGAGATCTCTCCATGCTGTGAGCAAGA 1118
QY 618 TGAAGGAGAGCGCGGAGCGCTACTTGGCCGAGCCCGGTGAAGCAGCGAGTGATCACCGTGC 677
Db 1119 TGAAGGAGAGCGCGGAGCGCTACTTGGCCGAGCCCGGTGAAGCAGCGAGTGATCACCGTGC 1178
QY 678 CC 679
Db 1179 CC 1180
RESULT 5
US-10-765-700-72
; Sequence 72, Application US/10765700
; Publication No. US20050130171A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/10/765,700
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/566,921
; PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 72
; LENGTH: 2962
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 349676.8
US-10-765-700-72
Query Match 17.3%; Score 431; DB 10; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3e-216;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 198 CCGTGGCTCCAGCTCCGACAGAGCTTCAGCCATGCGGCGCCAGCGGAGCTCGCGG 257
Db 699 CCGTGGCTCCAGCTCCGACAGAGCTTCAGCCATGCGGCGCCAGCGGAGCTCGCGG 758
QY 258 TGGGCATCGACCTGGGCGACACCTACTCTGCTGGTGGGCGTGTTCAGCAGGCGCGGTGG 317
Db 759 TGGGCATCGACCTGGGCGACACCTACTCTGCTGGTGGGCGTGTTCAGCAGGCGCGGTGG 818
QY 318 AGATCTCTGGCCACGACGAGGGCAACCGGACGACCGCCAGCTACGTGGGCTTCACCGACA 377
Db 819 AGATCTCTGGCCACGACGAGGGCAACCGGACGACCGCCAGCTACGTGGGCTTCACCGACA 878
QY 378 CCGAGCGGCTGGTGGGAGCGCGGCAAGAGCGGCGCCCTGAACCCCGCCACACCG 437
Db 879 CCGAGCGGCTGGTGGGAGCGCGGCAAGAGCGGCGCCCTGAACCCCGCCACACCG 938
QY 438 TGTTCGATGCAAGCGGCTGATCGGGCGCAAGTTCCGCGGACACCA CGGTGCGATCGGACA 497
Db 939 TGTTCGATGCAAGCGGCTGATCGGGCGCAAGTTCCGCGGACACCA CGGTGCGATCGGACA 998
QY 498 TGAAGCACTGGCCCTTCAGGTGTGTAGCGGCGCGCAAGCGGCGCGGTGCGGTATGCT 557
Db 999 TGAAGCACTGGCCCTTCAGGTGTGTAGCGGCGCGCAAGCGGCGCGGTGCGGTATGCT 1058
QY 558 ACCCGGGGAGGACAGACGTTCTTACCCCGAGGAGATCTCTCCATGCTGTGAGCAAGA 617
Db 1059 ACCCGGGGAGGACAGACGTTCTTACCCCGAGGAGATCTCTCCATGCTGTGAGCAAGA 1118
QY 618 TGAAGGAGAGCGCGGAGCGCTACTTGGCCGAGCCCGGTGAAGCAGCGAGTGATCACCGTGC 677
Db 1119 TGAAGGAGAGCGCGGAGCGCTACTTGGCCGAGCCCGGTGAAGCAGCGAGTGATCACCGTGC 1178

QY 678 CC 679
Db 1179 CC 1180
RESULT 6
US-10-637-855-217/c
; Sequence 217, Application US/10637855
; Publication No. US20040110194A1
; GENERAL INFORMATION:
; APPLICANT: Sornasse, Thierry
; APPLICANT: Cocks, Ben
; APPLICANT: Sanjwala, Bharati
; TITLE OF INVENTION: GENES REGULATED BY HUMAN CYTOKINES
; FILE REFERENCE: PA-0020 US
; CURRENT APPLICATION NUMBER: US/10/637,855
; CURRENT FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PERL Program
; SEQ ID NO 217
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1452827T6
US-10-637-855-217
Query Match 17.2%; Score 429; DB 8; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.6e-215;
Matches 429; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2024 GGAGCTGGAGCAAACTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCGCTGTGTGCC 2083
Db 429 GGAGCTGGAGCAAACTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCGCTGTGTGCC 370
QY 2084 TGGGGGCGAGCAGTTGTAGCGCTCAAGCCCAACAGGGGGAGCCCGAGCACCGGCCCATCAT 2143
Db 369 TGGGGGCGAGCAGTTGTAGCGCTCAAGCCCAACAGGGGGAGCCCGAGCACCGGCCCATCAT 310
QY 2144 TGAGGAGTTGATGTAATGGCCCTTCGTGATAGTCAGCTGTGACGTGTCAGGGCTATGCT 2203
Db 309 TGAGGAGTTGATGTAATGGCCCTTCGTGATAGTCAGCTGTGACGTGTCAGGGCTATGCT 250
QY 2204 ATGGGCTTCTAGACTGTCTTCTATGATCCTGCCCCTCAGAGATGAAGGGCTTGGGGGG 2263
Db 249 ATGGGCTTCTAGACTGTCTTCTATGATCCTGCCCCTCAGAGATGAAGGGCTTGGGGGG 190
QY 2264 TCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGTCTTTTACATTTTGGG 2323
Db 189 TCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGTCTTTTACATTTTGGG 130
QY 2324 GGGAGGGGGTTCATCTCTTCTGCTTCAAAATAAAAGTCATTAATTTTAAACCTGT 2383
Db 129 GGGAGGGGGTTCATCTCTTCTGCTTCAAAATAAAAGTCATTAATTTTAAACCTGT 70
QY 2384 GTGGCAGCTTTAAACATTCCTTTCACCTATAATTTGTGTATTTTGTACTTGTATGAA 2443
Db 69 GTGGCAGCTTTAAACATTCCTTTCACCTATAATTTGTGTATTTTGTACTTGTATGAA 10
QY 2444 TTTTGTAT 2452
Db 9 TTTTGTAT 1
RESULT 7
US-09-968-007A-527
; Sequence 527, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa

; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527
; LENGTH: 2492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-527

Query Match 13.2%; Score 329; DB 3; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCAACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGAGCTTCAGCCATGAGGCCCAACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 384
Qy 367 CTTTACCGACACCGAGCGGCTGCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 426
Db 385 CTTTACCGACACCGAGCGGCTGCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACACCAACG 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACACCAACG 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 8
US-10-278-698-290
; Sequence 290, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmüller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 2492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-290

Query Match 13.2%; Score 329; DB 9; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGCTTCAGCCATGAGGCCCAACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGCTTCAGCCATGAGGCCCAACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 384
Qy 367 CTTTACCGACACCGAGCGGCTGCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 426
Db 385 CTTTACCGACACCGAGCGGCTGCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACACCAACG 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACACCAACG 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 9
US-10-278-698-804
; Sequence 804, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmüller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 804
; LENGTH: 2492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-804

Query Match 13.2%; Score 329; DB 9; Length 2492;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGCTTCAGCCATGAGGCCCAACG 246
Db 205 GGCAGCAGCCTCCGTGGCCCTCCAGCATCCGACAGAGCTTCAGCCATGAGGCCCAACG 264
Qy 247 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 306
Db 265 GGAGCTCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 324
Qy 307 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 366
Db 325 GGGCCGCGTGGGATCTCGACCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 384
Qy 367 CTTTACCGACACCGAGCGGCTGCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 426
Db 385 CTTTACCGACACCGAGCGGCTGCTGGGCAACGACCACTACTCTGCTGGCGGTGTTTTCAGCA 444
Qy 427 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACACCAACG 486
Db 445 CCACAAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGCGACACCAACG 504

Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Dh 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 11

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US-10-755-889-395
; Sequence 395, Application US/107550889
; Publication NO. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755.889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 395
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-395

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Query Match	11.4%;	Score 283;	DB 8;	Length 1932;
Best Local Similarity	100.0%;	Prod. NO. 5e-138;		
Matches 283;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	233	ATGCAGGCCCCACGGGAGCTCGCGTGGGCATCGACCTGGGACCACTTACTCGTGGTG	292	
Db	1	ATGCAGGCCCCACGGGAGCTCGCGTGGGCATCGACCTGGGACCACTTACTCGTGGTG	60	
QY	293	GGCGTGTTCAGCAGGGCCGCTGGAGATCCTTGCCCAACGACCAAGGGCAACCGCACCAACG	352	
Db	61	GGCGTGTTCAGCAGGGCCGCTGGAGATCCTTGCCCAACGACCAAGGGCAACCGCACCAACG	120	
QY	353	CCACGCTACGTGGCTTTCACCGACACCGAGCGGTGTGTGGGAGCGCGCCNAGGCCAG	412	
Db	121	CCACGCTACGTGGCTTTCACCGACACCGAGCGGTGTGTGGGAGCGCGCCNAGGCCAG	180	
QY	413	GGGGCCCTGAACCCCCCAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTC	472	
Db	181	GGGGCCCTGAACCCCCCAACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTC	240	
QY	473	GGGGACACCAACCGTGGAGTCGGACATGAAGCACTGGCCCTTCC	515	
Db	241	GGGGACACCAACCGTGGAGTCGGACATGAAGCACTGGCCCTTCC	283	

RESULT 12

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1  RESULT 12
2  US-10-027-632-170807
3  ; Sequence 170807, Application US/10027632
4  ; Publication NO. US20020198371A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Wang, David G.
7  ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
8  ; Polymorphisms in the Human Genome
9  ; FILE REFERENCE: 108827,129
10 ; CURRENT APPLICATION NUMBER: US/10/027,632
11 ; CURRENT FILING DATE: 2002-04-30
12 ; PRIOR APPLICATION NUMBER: US 60/218,006
13 ; PRIOR FILING DATE: 2000-07-12
14 ; PRIOR APPLICATION NUMBER: US 60/198,676
15 ; PRIOR FILING DATE: 2000-04-20
16 ; PRIOR APPLICATION NUMBER: US 60/193,483
17 ; PRIOR FILING DATE: 2000-03-29
18 ; PRIOR APPLICATION NUMBER: US 60/185,218
19 ; PRIOR FILING DATE: 2000-02-24
20 ; PRIOR APPLICATION NUMBER: US 60/167,363

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Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
|||||
Dh 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 10

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US-10-843-641A-6997
; Sequence 6997, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0

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/ SOFTWARE: PATENTLIII VERSION 3.0
/ SEQ ID NO 6997
/ LENGTH: 2492
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(2492)
/ OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-6997

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Query Match	13.2%;	Score 329;	DB 10;	Length 2492;
Best Local Similarity	100.0%;	Pred. No. 2.5e-162;		
Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	187	GGCAGAGCCTCGTGGCTCCAGCATCCGACAAAGAAGCTTCAGCCATTCAGAGGCCCCACG	243
Db	205	GGCAGAGCCTCGTGGCTCCAGCATCCGACAAAGAAGCTTCAGCCATTCAGAGGCCCCACG	264
Qy	247	GGAGCTCGCGTGGGATCGA CTTGGGCAACCA CTTACTCTGCTGGTGGCGGTGTTTCAGCA	306
Db	265	GGAGCTCGCGTGGGATCGA CTTGGGCAACCA CTTACTCTGCTGGTGGCGGTGTTTCAGCA	324
Qy	307	GGGCGCGTGGAGATCTGGCCAAACGACAGGGCAACCGGACA CAGCCCAGCTACGTGGC	366
Db	325	GGGCGCGTGGAGATCTGGCCAAACGACAGGGCAACCGGACA CAGCCCAGCTACGTGGC	384
Qy	367	CTTCACGGACACAGAGCGGCTGGTTCGGGACCGGGCAAGAGCCAGCGCGGCCCTGAAACC	426
Db	385	CTTCACCGACACAGAGCGGCTGGTTCGGGACCGGGCAAGAGCCAGCGCGGCCCTGAAACC	444
Qy	427	CCACAAACCGTGTTCATGCCAAGGGCTGATCGGGCGCAAGTTCGCGGACACACACGCT	486
Db	445	CCACAAACCGTGTTCATGCCAAGGGCTGATCGGGCGCAAGTTCGCGGACACACACGCT	504

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; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170807
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-170807
```

```
Query Match 10.4%; Score 260; DB 6; Length 819;
Best Local Similarity 99.3%; Pred. No. 7.3e-126;
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 825 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTGCGTTCTCTCATTTGAGCGCGGTG 884
Db 49 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTGCGTTCTCTCATTTGAGCGGTG 108

QY 885 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAACC 944
Db 109 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAACC 168

QY 945 GGCTCGTGAACCACTTCATGGAAGAAATTCGGGCGGAAGCATGGGAAGGACCTGAGCGGGA 1004
Db 169 GGCTCGTGAACCACTTCATGGAAGAAATTCGGGCGGAAGCATGGGAAGGACCTGAGCGGGA 228

QY 1005 ACAAGCGTGCCTGGCAGAGCTGGCCACAGCTGTGAGCGCGCCAGCGCACCCCTGCT 1064
Db 229 ACAAGCGTGCCTGGCAGAGCTGGCCACAGCTGTGAGCGCGCCAGCGCACCCCTGCT 288

QY 1065 CCAGCACCCAGGCGCACCTCGGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 1124
Db 289 CCAGCACCCAGGCGCACCTCGGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 348

QY 1125 CCATCACTCGTCCCGCTTTGAGGAACTGTGCTCAGACCTTTCGCGCAGCACCTCGGAGC 1184
Db 349 CCATCACTCGTCCCGCTTTGAGGAACTGTGCTCAGACCTTTCGCGCAGCACCTCGGAGC 408

QY 1185 CGGTGGAGAGGCGCTCGGGATGCCAAGCTGCAAGGCCAGATTCATGAC 1237
Db 409 CGGTGGAGAGGCGCTCGGGATGCCAAGCTGCAAGGCCAGATTCATGAC 461
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```
RESULT 13
US-10-027-632-170807
; Sequence 170807, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 170807
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-170807

Query Match 10.4%; Score 260; DB 7; Length 819;
Best Local Similarity 99.3%; Pred. No. 7.3e-126;
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 825 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTGCGTTCTCTCATTTGAGCGCGGTG 884
Db 49 TCATTTTGGACCTGGGTGGGGGACCTTCGATGTGTGCGTTCTCTCATTTGAGCGGTG 108

QY 885 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAACC 944
Db 109 TCCTTTGAGGTGAAGCCACTGCTGGAGATACCCACCTGGGAGGAGGACTTCGACAACC 168

QY 945 GGCTCGTGAACCACTTCATGGAAGAAATTCGGGCGGAAGCATGGGAAGGACCTGAGCGGGA 1004
Db 169 GGCTCGTGAACCACTTCATGGAAGAAATTCGGGCGGAAGCATGGGAAGGACCTGAGCGGGA 228

QY 1005 ACAAGCGTGCCTGGCAGAGCTGGCCACAGCTGTGAGCGCGCCAGCGCACCCCTGCT 1064
Db 229 ACAAGCGTGCCTGGCAGAGCTGGCCACAGCTGTGAGCGCGCCAGCGCACCCCTGCT 288

QY 1065 CCAGCACCCAGGCGCACCTCGGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 1124
Db 289 CCAGCACCCAGGCGCACCTCGGAGATAGACTCCCTGTTTCGAGGCGCTGGACTTCTACAAGT 348

QY 1125 CCATCACTCGTCCCGCTTTGAGGAACTGTGCTCAGACCTTTCGCGCAGCACCTCGGAGC 1184
Db 349 CCATCACTCGTCCCGCTTTGAGGAACTGTGCTCAGACCTTTCGCGCAGCACCTCGGAGC 408

QY 1185 CGGTGGAGAGGCGCTCGGGATGCCAAGCTGCAAGGCCAGATTCATGAC 1237
Db 409 CGGTGGAGAGGCGCTCGGGATGCCAAGCTGCAAGGCCAGATTCATGAC 461
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RESULT 14
US-09-925-065A-12443/C
; Sequence 12443, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12443
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-12443
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Query Match 10.4%; Score 259; DB 4; Length 397;
Best Local Similarity 99.7%; Pred. No. 2.5e-125;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1263 CGCATCCCCCAGGTGCAGAAAGTTGCTGCAGGAGCTTCTTCAACGCGCAAGGAGCTGAACAAG 1322
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Db 356 CGCATCCCCAAGGTGCAGAAAGTTGCTGCAGGAATTCTTCAACGCGCAAGGAGCTGAACAAG 297
Qy 1323 AGCATCAACCTGATGAGGCTGTGGCTATGGGTCTGCTGCAGCGCGCGTGTGATG 1382
Db 296 AGCATCAACCTGATGAGGCTGTGGCTATGGGCTGCTGTGCAGCGCGCGTGTGATG 237
Qy 1383 GGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGGATGTGGCTCCCTGTCTCTG 1442
Db 236 GGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGGATGTGGCTCCCTGTCTCTG 177
Qy 1443 GGGCTGAGAGCAGCAGGTGGGCTGATGACACGCTGATCCAGAGAACGCCACTATCCCC 1502
Db 176 GGGCTGAGAGCAGCAGGTGGGCTGATGACACGCTGATCCAGAGAACGCCACTATCCCC 117
Qy 1503 ACCAAGCAGACCCAGACTTTTCCACCCTACTTCGACCAACAGCCTGGGCTCTTCATCCAG 1562
Db 116 ACCAAGCAGACCCAGACTTTTCCACCCTACTTCGACCAACAGCCTGGGCTCTTCATCCAG 57
Qy 1563 GTGTATGAGG 1572
Db 56 GTGTATGAGG 47

RESULT 15
US-09-925-065A-12443/c
; Sequence 12443, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12443
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-12443

Query Match 10.4%; Score 259; DB 5; Length 397;
Best Local Similarity 99.7%; Pred. No. 2.5e-125;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1263 CGCATCCCCAAGGTGCAGAAAGTTGCTGCAGGACTTCTTCAACGCGCAAGGAGCTGAACAAG 1322
Db 356 CGCATCCCCAAGGTGCAGAAAGTTGCTGCAGGACTTCTTCAACGCGCAAGGAGCTGAACAAG 297
Qy 1323 AGCATCAACCTGATGAGGCTGTGGCTATGGGTCTGCTGTGCAGCGCGCGTGTGATG 1382
Db 296 AGCATCAACCTGATGAGGCTGTGGCTATGGGCTGCTGTGCAGCGCGCGTGTGATG 237
Qy 1383 GGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGGATGTGGCTCCCTGTCTCTG 1442
Db 236 GGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGTGGATGTGGCTCCCTGTCTCTG 177
Qy 1443 GGGCTGAGAGCAGCAGGTGGGCTGATGACACGCTGATCCAGAGAACGCCACTATCCCC 1502
Db 176 GGGCTGAGAGCAGCAGGTGGGCTGATGACACGCTGATCCAGAGAACGCCACTATCCCC 117

Qy 1503 ACCAAGCAGACCCAGACTTTTCCACCCTACTTCGACCAACAGCCTGGGCTCTTCATCCAG 1562
Db 116 ACCAAGCAGACCCAGACTTTTCCACCCTACTTCGACCAACAGCCTGGGCTCTTCATCCAG 57
Qy 1563 GTGTATGAGG 1572
Db 56 GTGTATGAGG 47

Search completed: November 3, 2006, 23:12:53
Job time : 3383.41 secs

GenCore version 5.1.9
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OLM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 21:32:07 ; Search time 519.48 Seconds
(without alignments)
9311.708 Million cell updates/sec

Title: US-10-764-316-7
Perfect score: 2493
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2461376 seqs, 970166171 residues

Word size : 1

Total number of hits satisfying chosen parameters: 4922276

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:
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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2493	100.0	2493	6	US-10-764-316-7
2	519	20.8	1276	8	US-11-266-748A-183816
3	519	20.8	1276	8	US-11-266-748A-20242
4	400	16.0	702	8	US-11-266-748A-100981
5	400	16.0	702	8	US-11-266-748A-153792
6	283	11.4	1932	6	US-10-511-937-2830
7	227	9.1	777	8	US-11-266-748A-358486
8	227	9.1	777	8	US-11-266-748A-41865
9	187	7.5	445	6	US-10-834-268-4047
10	187	7.5	445	6	US-11-266-748A-52935
11	187	7.5	1000	8	US-11-266-748A-221107
12	187	7.5	1000	8	US-11-266-748A-395612
13	187	7.5	1000	8	US-11-266-748A-466658
14	167	6.7	559	8	US-11-266-748A-13932
15	143	5.7	682	8	US-11-266-748A-56036
16	120	4.8	968	6	US-10-764-316-9
17	100	4.0	729	8	US-11-266-748A-391479
18	100	4.0	729	8	US-11-266-748A-482197
19	91	3.7	445	6	US-10-834-268-4097
20	50	2.0	50	6	US-10-511-937-2661
21	38	1.5	1817	8	US-11-293-697-2173
22	38	1.5	2496	8	US-11-266-748A-30574
23	34	1.4	391	8	US-11-266-748A-169838

24	34	1.4	951	8	US-11-266-748A-381019	Sequence 381019,
25	34	1.4	951	8	US-11-266-748A-430773	Sequence 430773,
26	34	1.4	957	8	US-11-266-748A-23277	Sequence 23277, A
27	34	1.4	960	8	US-11-266-748A-184820	Sequence 184820,
28	34	1.4	960	8	US-11-266-748A-192321	Sequence 192321,
29	34	1.4	1119	8	US-11-266-748A-251463	Sequence 251463,
30	34	1.4	1119	8	US-11-266-748A-275460	Sequence 275460,
31	34	1.4	1119	8	US-11-266-748A-311980	Sequence 311980,
32	34	1.4	1613	8	US-11-266-748A-184822	Sequence 184822,
33	34	1.4	1613	8	US-11-266-748A-192323	Sequence 192323,
34	34	1.4	2563	8	US-11-266-748A-251465	Sequence 251465,
35	34	1.4	2563	8	US-11-266-748A-275462	Sequence 275462,
36	34	1.4	2563	8	US-11-266-748A-311982	Sequence 311982,
37	34	1.4	5387	6	US-10-517-441-111	Sequence 111, App
38	34	1.4	4647455	6	US-10-641-321-205	Sequence 205, App
39	33	1.3	2152	6	US-10-953-349-38921	Sequence 38921, A
40	33	1.3	2152	9	US-11-056-355B-1264	Sequence 1264, Ap
41	33	1.3	2168	9	US-11-174-307B-4949	Sequence 4949, Ap
42	29	1.2	813	9	US-11-218-305-2522	Sequence 2522, Ap
43	29	1.2	2315	6	US-10-953-349-31228	Sequence 31228, A
44	28	1.1	924	8	US-11-266-748A-184821	Sequence 184821,
45	28	1.1	924	8	US-11-266-748A-192322	Sequence 192322,

ALIGNMENTS

RESULT 1

US-10-764-316-7
; Sequence 7, Application US/10764316
; Publication No. US20060127359A1
; GENERAL INFORMATION:
; APPLICANT: BORRELLI, MICHAEL J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT ACTIVATED GENE
; FILE REFERENCE: 10546-109
; CURRENT APPLICATION NUMBER: US/10/764,316
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,473
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 2493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-316-7

Query Match	100.0%;	Score 2493;	DB 6;	Length 2493;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2493;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCCCGGCGCGCGCGCGGAGGCTTCGACTGGCGCGGAAAGGTCGGGAAAGGTTTCGGCGCG 60		
DB	1	CCCCGGCGCGCGCGCGGAGGCTTCGACTGGCGCGGAAAGGTCGGGAAAGGTTTCGGCGCG 60		
QY	61	GGCGGGTCCGGGAGGTGCAAAAGGATGAAACCCGTCGAAAGCGGAGCTGACGACATCCG 120		
DB	61	GGCGGGTCCGGGAGGTGCAAAAGGATGAAACCCGTCGAAAGCGGAGCTGACGACATCCG 120		
QY	121	AGCCGGGCTGGCGCGCAGAGAAACCGCAGGAGAGCTCTACTGTGAGCGCCCTCCGACCG 180		
DB	121	AGCCGGGCTGGCGCGCAGAGAAACCGCAGGAGAGCTCTACTGTGAGCGCCCTCCGACCG 180		
QY	181	CGGAGCGGAGCAGGCTCCGTCGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 240		
DB	181	CGGAGCGGAGCAGGCTCCGTCGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 240		
QY	241	CCGAGCGGAGCTCCGCGTGGGATGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGT 300		
DB	241	CCGAGCGGAGCTCCGCGTGGGATGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGT 300		
QY	301	TCAGAGGCGCGCTGGAGATCTTGGCCAAACGACGAGGCGCAACCGCAGCCAGCTA 360		

Db 301 TCAGCAGGGCGCGTGGAGATCTTGGCCAAACGACACAGGGCAACCGCAACCGCCAGCTA 360
Qy 361 CGTGGCTTCAACGACACAGCGCGCTGTGTGGGAGACGCGGCAAGAGCGAGCGCGCCCT 420
Db 361 CGTGGCTTCAACGACACAGCGCGCTGTGTGGGAGACGCGGCAAGAGCGAGCGCGCCCT 420
Qy 421 GAAACCCCAACACCGTGTGATGCAAGCGGCTGTGTGGGAGACGCGGCAAGAGCGAGCG 480
Db 421 GAAACCCCAACACCGTGTGATGCAAGCGGCTGTGTGGGAGACGCGGCAAGAGCGAGCG 480
Qy 481 CACGGTCGATCGGACATGAGCACTGCGCCCTTCCAGGTGTGTGGGAGACGCGGCAAGCG 540
Db 481 CACGGTCGATCGGACATGAGCACTGCGCCCTTCCAGGTGTGTGGGAGACGCGGCAAGCG 540
Qy 541 CAAAGTCGCTATGCTACCGCGGGAGGACAAGCGTTCCTACCGGAGGAGATCTCCTC 600
Db 541 CAAAGTCGCTATGCTACCGCGGGAGGACAAGCGTTCCTACCGGAGGAGATCTCCTC 600
Qy 601 CATGTGCTGAGCAAGATGAGGAGACGCGCGGCGCTTCTGGCCAGCGCCGCTGAAGCA 660
Db 601 CATGTGCTGAGCAAGATGAGGAGACGCGCGGCGCTTCTGGCCAGCGCCGCTGAAGCA 660
Qy 661 CGCAGTGATCACCGTCCCACTATTTCAAGTAACTCGCAGCGCGAGCGCCACCAAGGAGCG 720
Db 661 CGCAGTGATCACCGTCCCACTATTTCAAGTAACTCGCAGCGCGAGCGCCACCAAGGAGCG 720
Qy 721 GGGGGCCATTCGGGGCTCAAGGTCTGCGATCATCAATGAGGCCACGCGCAGCGCCAT 780
Db 721 GGGGGCCATTCGGGGCTCAAGGTCTGCGATCATCAATGAGGCCACGCGCAGCGCCAT 780
Qy 781 CGCCTATGGCTGAGACCGCGGGCGCGGGAAGCGCAACGCTGCTATTTTGAACCTGGG 840
Db 781 CGCCTATGGCTGAGACCGCGGGCGCGGGAAGCGCAACGCTGCTATTTTGAACCTGGG 840
Qy 841 TGGGGGCACTTCGATGTGTGGTCTTCCATTGACGCGCGTCTTTGAGGTGAAGC 900
Db 841 TGGGGGCACTTCGATGTGTGGTCTTCCATTGACGCGCGTCTTTGAGGTGAAGC 900
Qy 901 CATCTGGAGATACCCCTGGGAGGAGAGACTTTCGACAAACCGGCTCGTGAACCACTT 960
Db 901 CATCTGGAGATACCCCTGGGAGGAGAGACTTTCGACAAACCGGCTCGTGAACCACTT 960
Qy 961 CATGGAAAGATTCGGCGGAAGCATGGGAAGGACCTGAGCGGGAACAGCGTCCCTCG 1020
Db 961 CATGGAAAGATTCGGCGGAAGCATGGGAAGGACCTGAGCGGGAACAGCGTCCCTCG 1020
Qy 1021 CAGGCTGGCAGACCTGAGCGGCGCAAGCGCACCCGCTCTCCAGCACCCAGGCCAC 1080
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Qy 1081 CCTGGAGATAGACTCCCTGTTCGAGGCGGTGGAATTCATCAAGTCCATCTCTGTCGCG 1140
Db 1081 CCTGGAGATAGACTCCCTGTTCGAGGCGGTGGAATTCATCAAGTCCATCTCTGTCGCG 1140
Qy 1141 CTTTGAGAACTGTGCTCAGACCTTTCGCGAGCACCTCGAGCGCGGTGAGAGGCGCT 1200
Db 1141 CTTTGAGAACTGTGCTCAGACCTTTCGCGAGCACCTCGAGCGCGGTGAGAGGCGCT 1200
Qy 1201 GCGGATGCCAGCTGGACAAGGCCAGATTCATGACTTCGTCTGGGGGAGGGCTCCA 1260
Db 1201 GCGGATGCCAGCTGGACAAGGCCAGATTCATGACTTCGTCTGGGGGAGGGCTCCA 1260
Qy 1261 CTCGCATCCCCAAGGTGAGAACTGTGCGAGGACTTCTCAAGCGCAAGAGCTGAACA 1320
Db 1261 CTCGCATCCCCAAGGTGAGAACTGTGCGAGGACTTCTCTCAAGCGCAAGAGCTGAACA 1320
Qy 1321 AGGAGATCAACCTGATGAGGCTGTGGCTATGCGTCTGCTGTCAGCGCGCGCTGTGA 1380
Db 1321 AGGAGATCAACCTGATGAGGCTGTGGCTATGCGTCTGCTGTCAGCGCGCGCTGTGA 1380
Qy 1381 TGGGGGACAAATGTGAGAAAGTGCAGGATCTCTCTGCTGGAGTGGCTCCCTGCTC 1440

Db 1381 TGGGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGCTGATGTGGCTCCCTGTCTC 1440
Qy 1441 TGGGGCTGGAGACAGCAGGTGGGTGATGACCACTGATCCAGAGGACGCACTATCC 1500
Db 1441 TGGGGCTGGAGACAGCAGGTGGGTGATGACCACTGATCCAGAGGAAACGCACTATCC 1500
Qy 1501 CCACCAAGCAGACCCAGACTTTCACCACTTCTCGGCAACACAGCCTGGGGCTTTCATCC 1560
Db 1501 CCACCAAGCAGACCCAGACTTTCACCACTTCTCGGCAACACAGCCTGGGGCTTTCATCC 1560
Qy 1561 AGGTGTATGAGTTGAGAGGCGCATGACCAAGGACCAACCTGCTGGGGCTTTGAAC 1620
Db 1561 AGGTGTATGAGTTGAGAGGCGCATGACCAAGGACCAACCTGCTGGGGCTTTGAAC 1620
Qy 1621 TCATTGGCATCCCTCTGCGCCCATGAGTCCCCAGATAGAGGTGACGCTTTGACATTG 1680
Db 1621 TCATTGGCATCCCTCTGCGCCCATGAGTCCCCAGATAGAGGTGACGCTTTGACATTG 1680
Qy 1681 ATGCTAATGGCATCTGAGCGTGACGCCACTGACAGGAGCAGGTAAAGCTTAACAAGA 1740
Db 1681 ATGCTAATGGCATCTGAGCGTGACGCCACTGACAGGAGCAGGTAAAGCTTAACAAGA 1740
Qy 1741 TCACCAATGACAAAGCGCGCTGAGCAAGGAGGAGTGGAGGATGGTTTCATGAAGCGG 1800
Db 1741 TCACCAATGACAAAGCGCGCTGAGCAAGGAGGAGTGGAGGATGGTTTCATGAAGCGG 1800
Qy 1801 AGCAGTACGGGCTGAGGATGAGGCCAGAGGAGCAGAGTGGCTGCCAAAACCTCGCTGG 1860
Db 1801 AGCAGTACGGGCTGAGGATGAGGCCAGAGGAGCAGAGTGGCTGCCAAAACCTCGCTGG 1860
Qy 1861 AGGCCCATGTCTTCATGTGAAAGTCTTTGCAAGAGGAAAGCCTTAGGGAACAAGATTC 1920
Db 1861 AGGCCCATGTCTTCATGTGAAAGTCTTTGCAAGAGGAAAGCCTTAGGGAACAAGATTC 1920
Qy 1921 CCGAAGAGCAGAGCGCAAGGTGCAAGCAAGTGTCAAGAGTCTTGCCTGGCTGGAGC 1980
Db 1921 CCGAAGAGCAGAGCGCAAGGTGCAAGCAAGTGTCAAGAGTCTTGCCTGGCTGGAGC 1980
Qy 1981 ACAACAGCTGGCAGAGAGGAGATGAGCATCAGAGGAGGAGCTGGAGCAAACTCT 2040
Db 1981 ACAACAGCTGGCAGAGAGGAGATGAGCATCAGAGGAGGAGCTGGAGCAAACTCT 2040
Qy 2041 GTGCGCCCATCTTCTCCAGGCTCTATGGGGGGCTGTGCTCCCTGGGGGAGAGCTGTA 2100
Db 2041 GTGCGCCCATCTTCTCCAGGCTCTATGGGGGGCTGTGCTCCCTGGGGGAGAGCTGTA 2100
Qy 2101 GCGCTCAAGCCCAACAGGCGGACCCAGCAACCGGCCCATCATTTGAGGAGGTTGATGAA 2160
Db 2101 GCGCTCAAGCCCAACAGGCGGACCCAGCAACCGGCCCATCATTTGAGGAGGTTGATGAA 2160
Qy 2161 TGGCCCTTCTGATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2220
Db 2161 TGGCCCTTCTGATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2220
Qy 2221 TCTTCTATGATCTCCCTTCAGAGATGAAGGCTTGGGGGGCTTCCCTCCAAAGCTA 2280
Db 2221 TCTTCTATGATCTCCCTTCAGAGATGAAGGCTTGGGGGGCTTCCCTCCAAAGCTA 2280
Qy 2281 GAACCTTCTTCCAGGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2340
Db 2281 GAACCTTCTTCCAGGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2340
Qy 2341 TCCTTCTGCTCAAAATGAAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2400
Db 2341 TCCTTCTGCTCAAAATGAAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2400
Qy 2401 CTTTCACTATATTTGTGATTTGTTACTGTATGATGATGATGATGATGATGATGATGATGATG 2460
Db 2401 CTTTCACTATATTTGTGATTTGTTACTGTATGATGATGATGATGATGATGATGATGATGATG 2460
Qy 2461 TAGTTATAGACCTAAATAAACTTTTAAAACTCC 2493
Db 2461 TAGTTATAGACCTAAATAAACTTTTAAAACTCC 2493

RESULT 2
US-11-266-748A-183816/c
; Sequence 183816, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 183816
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1065)..(1090)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-183816

Query Match 20.8%; Score 519; DB 8; Length 1276;
Best Local Similarity 99.7%; Pred. No. 2.5e-251;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGCGGGCGGGAGGCTCTCGACTGGGCGGGAAGGTTCGGGAAGGTTTCGGGCG 60
DB 726 CCCGGCGGGCGGGAGGCTCTCGACTGGGCGGGAAGGTTCGGGAAGGTTTCGGGCG 667

QY 61 GCGGGGTTCGGGAGGTGCAAAAGGATGAAAGCCCGTGGAGCGGAGCTGAGCAGATCCG 120
DB 666 GCGGGGTTCGGGAGGTGCAAAAGGATGAAAGCCCGTGGAGCGGAGCTGAGCAGATCCG 607

QY 121 AGCGGGCTTCGGCGCAGAGAAACCGCAGGAGAGGCTCTCACTGTGAGCGCCCTCCAGCG 180
DB 606 AGCGGGCTTCGGCGCAGAGAAACCGCAGGAGAGGCTCTCACTGTGAGCGCCCTCCAGCG 547

QY 181 CGGAGCGGAGCAGCCTTCCTGGGCTCCAGATCCGACAAAGAGCTTCAGCCATCAGGC 240
DB 546 CGGAGCGGAGCAGCCTTCCTGGGCTCCAGATCCGACAAAGAGCTTCAGCCATCAGGC 487

QY 241 CCCACGGAGCTCGCGTGGGCTTCGACCTGGGCAACCACTTACTCTGCTGGGCTGGT 300
DB 486 CCCACGGAGCTCGCGTGGGCTTCGACCTGGGCAACCACTTACTCTGCTGGGCTGGT 427

QY 301 TCAGCAGGCGCGGCTGGAGATCTCTGGCCAAACGACCGAGGCAACCGACACCGCCAGCTA 360
DB 426 TCAGCAGGCGCGGCTGGAGATCTCTGGCCAAACGACCGAGGCAACCGACACCGCCAGCTA 367

QY 361 CGTGCGCTTCACCGACACCGAGCGGTGGTTCGGGAGCGCGCCCAAGAGCGCGGCCCT 420
DB 121 AGCGGGGTTCGGGAGGAGAAACCGCAGGAGAGCTCACTGCTGAGCGGCCCTTCGACCG 180

DB 366 CGTGGCTTCACCGACACGAGCGGCTGGTTCGGGAGCGGGCCCAAGAGCGCGGCCCT 307
QY 421 GAACCCCAACACACCGTTCGATGCCCAAGCGGCTGATCGGCGCAAGTTTCGGGACAC 480
DB 306 GAACCCCAACACACCGTTCGATGCCCAAGCGGCTGATCGGCGCAAGTTTCGGGACAC 247
QY 481 CACGGTGCAGTCCGACATGAAGCAGTGGCCCTTCCAGGTGGTGGAGCGGCGGCAAGCC 540
DB 246 CACGGTGCAGTCCGACATGAAGCAGTGGCCCTTCCAGGTGGTGGAGCGGCGGCAAGCC 187
QY 541 CACGGTGCAGTTCGATGCTACCGCGGAGGAGCAAGAGCTTACCCCGAGAGATTCGTC 600
DB 186 CAAAGTGCAGTATGCTACCGCGGAGGAGCAAGAGCTTACCCCGAGAGATTCGTC 127
QY 601 CATGGTGCAGCAAGATGAA 621
DB 126 CATGGTGCAGCAAGATGAA 106

RESULT 3
US-11-266-748A-240242
; Sequence 240242, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 240242
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (187)..(211)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-240242

Query Match 20.8%; Score 519; DB 8; Length 1276;
Best Local Similarity 99.7%; Pred. No. 2.5e-251;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGCGGGCGGGAGGCTCTCGACTGGGCGGGAAGGTTCGGGAAGGTTTCGGGCG 60
DB 551 CCCGGCGGGCGGGAGGCTCTCGACTGGGCGGGAAGGTTCGGGAAGGTTTCGGGCG 610

QY 61 GCGGGGTTCGGGAGGTGCAAAAGGATGAAAGCCCGTGGAGCGGAGCTGAGCAGATCCG 120
DB 611 GCGGGGTTCGGGAGGTGCAAAAGGATGAAAGCCCGTGGAGCGGAGCTGAGCAGATCCG 670

QY 121 AGCGGGGTTCGGGAGGAGAAACCGCAGGAGAGCTCACTGCTGAGCGGCCCTTCGACCG 180

Mon Nov 6 11:55:56 2006

Db 671 AGCGGGCTGGCGGCGAGAGAAACCGCAGGAGAGCTCACTGCTGAGCGCCCTCGACGG 730
Qy 181 CGGAGCGGCAAGCAGCTCCGTGGCCCTCCAGCATCCGACAAAGAGCTTCAGCCATGACGCG 240
Db 731 CGGAGCGGCAAGCAGCTCCGTGGCCCTCCAGCATCCGACAAAGAGCTTCAGCCATGACGCG 790
Qy 241 CCCACGGGAGCTCGCGTGGGCAATCGACCTGGGCAACCACTACTCTGCTGGGCGTGT 300
Db 791 CCCACGGGAGCTCGCGTGGGCAATCGACCTGGGCAACCACTACTCTGCTGGGCGTGT 850
Qy 301 TCACAGCGGCGCTGGAGATCTTGGGCAACGACGAGGCAACCGCACCAAGCCACGTA 360
Db 851 TCACAGCGGCGCTGGAGATCTTGGGCAACGACGAGGCAACCGCACCAAGCCACGTA 910
Qy 361 CGTGGCTTCCACGACACCGAGCGGCTGGTGGGGAACCGGCAAGAGCCAGCGGCGCT 420
Db 911 CGTGGCTTCCACGACACCGAGCGGCTGGTGGGGAACCGGCAAGAGCCAGCGGCGCT 970
Qy 421 GAACCCCAACACCGGCTGGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGCGGACAC 480
Db 971 GAACCCCAACACCGGCTGGATGCCAAGCGGCTGATCGGGCGCAAGTTCCGCGGACAC 1030
Qy 481 CACGGTGCAGTCGGACATGAAGCACTGGCCCTTCAGGTGTGACGAGGCGGCAAGCC 540
Db 1031 CACGGTGCAGTCGGACATGAAGCACTGGCCCTTCAGGTGTGACGAGGCGGCAAGCC 1090
Qy 541 CAAAGTGGCGTATCTACCGCGGGGAGGAGCAAGAGCTTCTACCCGAGGAGATCTCGTC 600
Db 1091 CAAAGTGGCGTATCTACCGCGGGGAGGAGCAAGAGCTTCTACCCGAGGAGATCTCGTC 1150
Qy 601 CATGGTGTGAGCAAGATGAA 621
Db 1151 CATGGTGTGAGCAAGATGAA 1171

RESULT 4
US-11-266-748A-100981
; Sequence 100981, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100981
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (61)..(61)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-100981
Query Match 16.0%; Score 400; DB 8; Length 702;
Best Local Similarity 99.6%; Pred. No. 3e-191;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1991 GGCAGAGAGGAGAGATGATGAGCATCAGAGAGGAGAGCTGGAGCAATCTGTGCGCCCAT 2050
Db 197 GGCAGAGAGGAGAGATGATGAGCATCAGAGAGGAGAGCTGGAGCAATCTGTGCGCCCAT 256
Qy 2051 CTTCTCCAGGCTCTATGGGGGCTGTGTCCCTGGGGGAGCAGCAAGTTGTAGCGCTCAAGC 2110
Db 257 CTTCTCCAGGCTCTATGGGGGCTGTGTCCCTGGGGGAGCAGCAAGTTGTAGCACTCAAGC 316
Qy 2111 CCACCAGGGGAGCCCGACCGCCCATCATATTGAGAGGTTGATTGAATGGCCCTTCG 2170
Db 317 CCACCAGGGGAGCCCGACCGCCCATCATATTGAGAGGTTGATTGAATGGCCCTTCG 376
Qy 2171 TGATAAGTCAGCTGTGACTGTGAGGCTATGCTATGGGCTTCTAGACTGTCTTCTATGA 2230
Db 377 TGATAAGTCAGCTGTGACTGTGAGGCTATGCTATGGGCTTCTAGACTGTCTTCTATGA 436
Qy 2231 TCCTGCCCTTCAGAGATGAAGGCTTGGGGGGTCTTCCCTCCAAAGCTAGAACTTTCTT 2290
Db 437 TCCTGCCCTTCAGAGATGAAGGCTTGGGGGGTCTTCCCTCCAAAGCTAGAACTTTCTT 496
Qy 2291 TCAGAGATGAAGTCTTTTGAATTTTAAACTTTTGGGGGAGGCGGTTCATCCCTTCTGCTT 2350
Db 497 CCAGAGATGAAGTCTTTTGAATTTTAAACTTTTGGGGGAGGCGGTTCATCCCTTCTGCTT 556
Qy 2351 CAAATATAAAGTCATTAATTTTAAACTTTTGGGCACTTTTAAACATTCGCTTTCACCTA 2410
Db 557 CAAATATAAAGTCATTAATTTTAAACTTTTGGGCACTTTTAAACATTCGCTTTCACCTA 616
Qy 2411 TATTTGTGTATTTGTTACTTGTATGATGAATTTGTTATGTAATAATATAGTTATAGA 2470
Db 617 TATTTGTGTATTTGTTACTTGTATGATGAATTTGTTATGTAATAATATAGTTATAGA 676
Qy 2471 CCTAATAAATCTTTTAAACTC 2492
Db 677 CCTAATAAATCTTTTAAACTC 698
RESULT 5
US-11-266-748A-153792/c
; Sequence 153792, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100981
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; PRIOR FILING DATE: 2005-07-18
;
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 153792
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo Sapiens
;
; FEATURE:
;
; NAME/KEY: misc_feature
; LOCATION: (642)..(642)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-153792

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Query Match	16.0%;	Score 400;	DB 8;	Length 702;
Best Local Similarity	99.6%;	Pred. No. 3e-191;		
Matches 500;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1991	GGCAGAGAAGGAGGAGTATGAGCATCAGAGAGGGAGCTGGAGCAAAATCTGTGCCCCCAT	2050	
DB	506	GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGGAGCTGGAGCAAAATCTGTGCCCCCAT	447	
QY	2051	CTTCTCCAGGCTCTATGGGGGGCCGTGTGTCCCTGGGGGCGAGCAGTGTGTAGCGCTCAAGC	2110	
DB	446	CTTCTCCAGGCTCTATGGGGGGCCGTGTGTCCCTGGGGGCGAGCAGTGTGTAGCACTCAAGC	387	
QY	2111	CCACCAGGGGGAGCCCCCAGCACCGGCCCCATCATTTGAGGAGGTTGATGAAATGGCCCTTCG	2170	
DB	386	CCACCAGGGGGAGCCCCCAGCACCGGCCCCATCATTTGAGGAGGTTGATGAAATGGCCCTTCG	327	
QY	2171	TGATAAGTCAGCTGTGACTGTCAAGGCTATGCTATGGGCCCTTCTAGACTGTCTCTATGA	2230	
DB	326	TGATAAGTCAGCTGTGACTGTCAAGGCTATGCTATGGGCCCTTCTAGACTGTCTCTATGA	267	
QY	2231	TCCTGCCCTTTCAGAGATGAAGGGCTTGGGGGGGTCTTCCCTCCAAAGCTAGAACTTTCTT	2290	
DB	266	TCCTGCCCTTTCAGAGATGAAGGGCTTGGGGGGGTCTTCCCTCCAAAGCTAGAACTTTCTT	207	
QY	2291	TCAGGATAACTGAAGCTTTTTCGACTTTTGGGGGGAGGGCGGTTCACTCTTCTGCTT	2350	
DB	206	CCCAGGATAACTGAAGCTTTTTCGACTTTTGGGGGGAGGGCGGTTCACTCTTCTGCTT	147	
QY	2351	CAAAATAAAGTCATTAATTTATTAATAACTTGTGTGCACCTTTAAACATTGCTTTACCTA	2410	
DB	146	CAAAATAAAGTCATTAATTTATTAATAACTTGTGTGCACCTTTAAACATTGCTTTACCTA	87	
QY	2411	TATTTTGTGTATTTTGTGTACTTGTATGTATGAATTTTGTATGTATGTAATATAGTTATAGA	2470	
DB	86	TATTTTGTGTATTTTGTGTACTTGTATGTATGAATTTTGTATGTATGTAATATAGTTATAGA	27	
QY	2471	CTTAAATAAACTTTTAAAACTC	2492	
DB	26	CCTAAATAAACTTTTAAAACTC	5	

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RESULT 6
US/10-511-937-2830
; Sequence 2830, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: AND MONITORING TREATMENT
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511.9
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/01

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; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2830
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2830

Query Match      11.4%; Score 283; DB 6; Length 1932;
Best Local Similarity 100.0%; Pred. No. 3.9e-132;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      233  ATGCAGAGCCCCACGGGAGCTCGCGGTGGGCATCGACCTGGGCGACCACTACTCTGTCGCGTG 292
Db      1   ATGCAGAGCCCCACGGGAGCTCGCGGTGGGCATCGACCTGGGCGACCACTACTCTGTCGCGTG 60

Qy      293  GGCGTGTTTCAGCAGGGGCCGCTGGAGATCTTGGCCAAACGACGAGGCAACCGCACCCAG 352
Db      61  GGCCTGTTTCAGCAGGGGCCGCTGGAGATCTTGGCCAAACGACGAGGCAACCGCACCCAG 120

Qy      353  CCCAGCTACGTGGCTTTCACCGACACCGAGCGGCTGGTCTGGGGAACGGGCCCAAGAGCCAG 412
Db      121  CCCAGCTACGTGGCTTTCACCGACACCGAGCGGCTGGTCTGGGGAACGGGCCCAAGAGCCAG 180

Qy      413  GCGGCCCTGAACCCGCCCAACACACCGTGTTTCGATGCCAAGCGCTCATCGGGCGCAAGTTC 472
Db      181  GCGGCCCTGAACCCGCCCAACACACCGTGTTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTC 240

Qy      473  GCGGACACCAAGGTGCGAGTCGGACATGAAGCACTGGCCCTTCC 515
Db      241  GCGGACACCAAGGTGCGAGTCGGACATGAAGCACTGGCCCTTCC 283

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RESULT 7
US-11-2666-748A-358486
; Sequence 358486, Application US/112666748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/2666,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 358486
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo Sapiens

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US-11-266-748A-358486	Query Match Best Local Similarity 9.1%; Score 227; DB 8; Length 777; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	2266	TTCCCTCCAAAGCTAGAACTTCTTTCCAGGATAACTGAAAGTCCTTTGACTTTTTCGGGG 2325		
DB	551	TTCCCTCCAAAGCTAGAACTTCTTTCCAGGATAACTGAAAGTCCTTTGACTTTTTCGGGG 610		
QY	2326	GAGGGCGGTTCATCCCTCTCTCTCAAAATAAAAAGTCATTAATTAATAAACTTGTGT 2385		
DB	611	GAGGGCGGTTCATCCCTCTCTCTCAAAATAAAAAGTCATTAATTAATAAACTTGTGT 670		
QY	2386	GGCAGCTTAAACATGCTTTTCACTATATTTTGTGTATTTTGTACTTTTGTATGTATGAATT 2445		
DB	671	GGCAGCTTAAACATGCTTTTCACTATATTTTGTGTATTTTGTACTTTTGTATGTATGAATT 730		
QY	2446	TTGTTATGTAAAAATATAGTTTATAGACCTAAATAAACTTTTAAAACTC 2492		
DB	731	TTGTTATGTAAAAATATAGTTTATAGACCTAAATAAACTTTTAAAACTC 777		
RESULT 8				
US-11-266-748A-441865/c				
; Sequence 441865, Application US/11266748A				
; Publication No. US20060134663A1				
; GENERAL INFORMATION:				
; APPLICANT: Harkin, Paul				
; APPLICANT: Johnston, Patrick				
; APPLICANT: Mulligan, Karl				
; TITLE OF INVENTION: Transcriptome Microarray Technology and				
; TITLE OF INVENTION: Methods of Using the Same				
; FILE REFERENCE: 59815-0102 (319189)				
; CURRENT APPLICATION NUMBER: US/11/266,748A				
; CURRENT FILING DATE: 2005-11-03				
; PRIOR APPLICATION NUMBER: EP 04105479.2				
; PRIOR FILING DATE: 2004-11-03				
; PRIOR APPLICATION NUMBER: EP 04105482.6				
; PRIOR FILING DATE: 2004-11-03				
; PRIOR APPLICATION NUMBER: EP 04105483.4				
; PRIOR FILING DATE: 2004-11-03				
; PRIOR APPLICATION NUMBER: EP 04105507.0				
; PRIOR FILING DATE: 2004-11-03				
; PRIOR APPLICATION NUMBER: EP 04105485.9				
; PRIOR FILING DATE: 2004-11-03				
; PRIOR APPLICATION NUMBER: EP 04105484.2				
; PRIOR FILING DATE: 2004-11-03				
; PRIOR APPLICATION NUMBER: US 60/662,276				
; PRIOR FILING DATE: 2005-03-14				
; PRIOR APPLICATION NUMBER: US 60/700,293				
; PRIOR FILING DATE: 2005-07-18				
; NUMBER OF SEQ ID NOS: 483996				
; SOFTWARE: PatentIn version 3.3				
; SEQ ID NO 441865				
; LENGTH: 777				
; TYPE: DNA				
; ORGANISM: Homo Sapiens				
US-11-266-748A-441865				
Query Match Best Local Similarity 9.1%; Score 227; DB 8; Length 777; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	2266	TTCCCTCCAAAGCTAGAACTTCTTTCCAGGATAACTGAAAGTCCTTTGACTTTTTCGGGG 2325		
DB	227	TTCCCTCCAAAGCTAGAACTTCTTTCCAGGATAACTGAAAGTCCTTTGACTTTTTCGGGG 168		
QY	2326	GAGGGCGGTTCATCCCTCTCTCTCAAAATAAAAAGTCATTAATTAATAAACTTGTGT 2385		
DB	167	GAGGGCGGTTCATCCCTCTCTCTCAAAATAAAAAGTCATTAATTAATAAACTTGTGT 108		
QY	2386	GGCAGCTTAAACATGCTTTTCACTATATTTTGTGTATTTTGTACTTTTGTATGTATGAATT 2445		

; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52935
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-52935

Query Match
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1811 GGCTGAGGATGAGGCCAGAGGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 1870
Db 98 GGCTGAGGATGAGGCCAGAGGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 157
Qy 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGACAAAGATTCCCGAAGAGGA 1930
Db 158 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGACAAAGATTCCCGAAGAGGA 217
Qy 1931 CAGCGCAAGTGAAGCAAGTGTGAGGAAGTCTTGGCTGGCTGGAGCACCAACAGCT 1990
Db 218 CAGCGCAAGTGAAGCAAGTGTGAGGAAGTCTTGGCTGGCTGGAGCACCAACAGCT 277
Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 2050
Db 278 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 337
Qy 2051 CTTCTCAGGCTCTATGGGGGCGCTGTGTGCTTCCCTGGGGGCGAGCAGTTGT 2099
Db 338 CTTCTCAGGCTCTATGGGGGCGCTGTGTGCTTCCCTGGGGGCGAGCAGTTGT 386

RESULT 11
US-11-266-748A-221107
; Sequence 221107, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52935
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-52935

; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 221107
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-221107

Query Match
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1811 GGCTGAGGATGAGGCCAGAGGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 1870
Db 333 GGCTGAGGATGAGGCCAGAGGAGGACAGAGTGGCTGCCAAAACCTCGCTGGAGGCCCATGT 392
Qy 1871 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGACAAAGATTCCCGAAGAGGA 1930
Db 393 CTTCCATGTGAAAGGTTCTTTGCAAGAGGAAAGGCTTTAGGACAAAGATTCCCGAAGAGGA 452
Qy 1931 CAGGCCCAAGTGAAGCAAGTGTGAGGAAGTCTTGGCTGGCTGGAGCACCAACAGCT 1990
Db 453 CAGGCCCAAGTGAAGCAAGTGTGAGGAAGTCTTGGCTGGCTGGAGCACCAACAGCT 512
Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 2050
Db 513 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 572
Qy 2051 CTTCTCAGGCTCTATGGGGGCGCTGTGTGCTTCCCTGGGGGCGAGCAGTTGT 2099
Db 573 CTTCTCAGGCTCTATGGGGGCGCTGTGTGCTTCCCTGGGGGCGAGCAGTTGT 621

RESULT 12
US-11-266-748A-395612
; Sequence 395612, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 395612
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-395612

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Query Match          7.5%; Score 187; DB 8; Length 1000;
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GGCTGAGGATGAGCCCGAGAGGACAGAGTGCGTGCACAAAATCTCGCTGGAGGCCCATGT 1870
DB 333 GGCTGAGGATGAGCCCGAGAGGACAGAGTGCGTGCACAAAATCTCGCTGGAGGCCCATGT 392

QY 1871 CTTCCATGTGAAGGTTCTTTGCAAGAGGAAGCCTTAGGAGCAAGATTCCCGAAGAGGA 1930
DB 393 CTTCCATGTGAAGGTTCTTTGCAAGAGGAAGCCTTAGGAGCAAGATTCCCGAAGAGGA 452

QY 1931 CAGGCGCAAGTCAAGCAAGTGTCAAGAGTCTTGGCAAGTCTTGGCTGGAGCAACACAGCT 1990
DB 453 CAGGCGCAAAATGCAAGCAAGTGTGCGGAAGTCTTGGCTGGAGCAACACAGCT 512

QY 1991 GGCAGAGAGGAGGATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 2050
DB 513 GGCAGAGAGGAGGATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 572

QY 2051 CTTCTCCAGGCTCTATGGGGGCGCTGGTGTCCCTGGGGGAGCAGATTGT 2099
DB 573 CTTCTCCAGGCTCTATGGGGGCGCTGGTGTCCCTGGGGGAGCAGATTGT 621

RESULT 13
US-11-266-748A-466658/c
; Sequence 466658, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 466658
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-466658

Query Match          7.5%; Score 187; DB 8; Length 1000;
Best Local Similarity 99.3%; Pred. No. 1.1e-83;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GGCTGAGGATGAGCCCGAGAGGACAGAGTGCGTGCACAAAATCTCGCTGGAGGCCCATGT 1870
DB 668 GGCTGAGGATGAGCCCGAGAGGACAGAGTGCGTGCACAAAATCTCGCTGGAGGCCCATGT 609

QY 1871 CTTCCATGTGAAGGTTCTTTGCAAGAGGAAGCCTTAGGAGCAAGATTCCCGAAGAGGA 1930
DB 608 CTTCCATGTGAAGGTTCTTTGCAAGAGGAAGCCTTAGGAGCAAGATTCCCGAAGAGGA 549
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QY 1931 CAGGCGCAAGTCAAGCAAGTGTCAAGAGTCTTGGCTGGAGCAACACAGCT 1990
DB 548 CAGGCGCAAAATGCAAGCAAGTGTGCGGAAGTCTTGGCTGGAGCAACACAGCT 489

QY 1991 GGCAGAGAGGAGGATGATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 2050
DB 488 GGCAGAGAGGAGGATGATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCAT 429

QY 2051 CTTCTCCAGGCTCTATGGGGGCGCTGGTGTCCCTGGGGGAGCAGATTGT 2099
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RESULT 14
US-11-266-748A-13932
; Sequence 13932, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13932
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-13932

Query Match          6.7%; Score 167; DB 8; Length 559;
Best Local Similarity 99.3%; Pred. No. 1.4e-73;
Matches 267; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1831 GGGACAGAGTGGCTGCCAAAATCTCGCTGGAGGCCCATGTCTCCATGTGAAGGTTCTT 1890
DB 5 GGGACAGAGTGGCTGCCAAAATCTCGCTGGAGGCCCATGTCTCCATGTGAAGGTTCTT 64

QY 1891 TGCAGAGGAGGAAGCCTTAGGGAGCAAGATTCCCGAAGAGGACAGCGCGCAAAAGTGCAGAGCA 1950
DB 65 TGCAGAGGAGGAAGCCTTAGGGAGCAAGATTCCCGAAGAGGACAGCGCGCAAAATGCAGAGCA 124

QY 1951 AGTGTCAAGGAAGTCTTGGCTGGAGCAACACAGCTGGCAGAGAGGAGGATATG 2010
DB 125 AGTGTGGGAAGTCTTGGCTGGAGCAACACAGCTGGCAGAGAGGAGGATATG 184

QY 2011 AGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCATCTTCTCCAGGCTCTATGGGG 2070
DB 185 AGCATCAGAGAGGAGCTGGAGCAAAATCTGTGCCCCCATCTTCTCCAGGCTCTATGGGG 244

QY 2071 GGCCTGGTGTCCCTGGGGGAGCAGATTGT 2099
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Db 245 GGCCTGGTGTCCCTGGGGGACAGCAGTTGT 273

RESULT 15

US-11-266-748A-56036
; Sequence 56036, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56036
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56036

Query Match 5.7%; Score 143; DB 8; Length 682;
Best Local Similarity 99.2%; Pred. No. 1.8e-61;
Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1811 GGCTGAGGATCAGGCCAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 1870
Db 109 GGCTGAGATGAGGCCAGAGGACAGAGTGGCTGCCAAAACTCGCTGGAGGCCCATGT 168
Qy 1871 CTTCCATGTGAAGGTTCTTTGCAAGAGGAAGCCTTAGGGAACAAGATCCCGAAGAGGA 1930
Db 169 CTTCCATGTGAAGGTTCTTTGCAAGAGGAAGCCTTAGGGAACAAGATCCCGAAGAGGA 228
Qy 1931 CAGGCGCAAGTGCAGACAAGTGTGAGGAAGTCTTGCTGGCTGGAGCACAACAGCT 1990
Db 229 CAGGCGCAAAATGCAAGACAAGTGTGCGGAAGTCTTGCTGGCTGGAGCACAACAGCT 288
Qy 1991 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTCGCCCAT 2050
Db 289 GGCAGAGAGGAGGAGTATGAGCATCAGAGAGGAGCTGGAGCAAAATCTGTCGCCCAT 348
Qy 2051 CTTCT 2055
Db 349 CTTCT 353

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Job time : 523.48 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 20:51:16 ; Search time 10960.4 Seconds
(without alignments)
12719.092 Million cell updates/sec

Title: US-10-764-316-7

Perfect score: 2493

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Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	660	26.5	764	3	BM677874
C 2	659	26.4	707	3	BU617655
C 3	632	25.4	936	3	BQ918107
C 4	624	25.0	709	9	DR004990
C 5	587	23.5	698	7	BF448220
C 6	582	23.3	676	4	CA426117
C 7	579	23.2	579	4	CA391777
C 8	564	22.6	1003	4	EX357704
C 9	535	21.5	537	1	AI652340
C 10	534	21.4	534	7	BF590626
C 11	512	20.5	567	9	DB017526
C 12	508	20.4	662	9	DA828714
C 13	503	20.2	852	3	BQ212261
C 14	499	20.0	575	1	AI636649
C 15	496	19.9	877	4	EX348810
C 16	495	19.9	570	9	DA877508
C 17	495	19.9	573	9	DB191153
C 18	495	19.9	574	9	DB123962
C 19	495	19.9	580	9	DA821617

20	495	19.9	581	9	DB112850
21	495	19.9	582	3	BP233047
22	495	19.9	582	9	DA143753
23	495	19.9	582	9	DB204579
24	495	19.9	583	3	BP208756
25	495	19.9	584	9	DB170275
26	495	19.9	589	9	DA389790
27	495	19.9	590	9	DA593582
28	495	19.9	600	9	DA941037
29	495	19.9	1056	2	BM546945
30	495	19.9	2878	6	CR623806
31	494	19.8	565	9	DB103143
32	493	19.8	564	9	DA594610
33	491	19.7	562	9	DA010341
34	490	19.7	561	9	DA592862
35	490	19.7	561	9	DB013313
36	486	19.5	591	9	DB200528
37	485	19.5	556	9	DB104556
38	476	19.1	547	9	DB127250
39	473	19.0	544	9	DB102455
40	472	18.9	543	9	DA963272
41	468	18.8	591	9	DB202792
42	467	18.7	518	9	DB208890
C 43	467	18.7	531	9	DB328896
44	467	18.7	538	9	DB117002
45	463	18.6	534	9	DA961155

ALIGNMENTS

BM677874 764 bp mRNA linear EST 27-FEB-2002
UI-E-EJ0-aie-l-08-0-UI-el UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-aie-l-08-0-UI 3', mRNA sequence.

BM677874.1 GI:18987770

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

1 (bases 1 to 764)

Ronaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa, 4156 MEBRF, Iowa City, IA 52242, USA

375 Newton Road,

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Forward

POLYA=yes.

Location/Qualifiers

1..764

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-EJ0-aie-l-08-0-UI"

/tissue_type="fetal eyes, lens, eye anterior segment,

optic nerve, retina, Retina Foveal and Macular, RPE and

Choroid"

/dev_stage="fetal and adult"

/lab_host="PH10B (Life Technologies) (T1 phase resistant)"

/clone_lib="UI-E-EJ0"

/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ0 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAGGA; lens, CGATTAGGGA; eye anterior segment, AATCCGCAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG TISSUE=human lens TAG_LIB=UI-E-EJ0 TAG_SEQ=CGATTAGGGA"

ORIGIN

Query Match 26.5%; Score 660; DB 3; Length 764;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1833 GACAGAGTGGTCCAAAACCTCGCTGGAGGCCATGCTTCCATGTGAAGTCTTTTG 1892

Db 678 GACAGAGTGGTCCAAAACCTCGCTGGAGGCCATGCTTCCATGTGAAGTCTTTTG 619

QY 1893 CAAGAGGAAGCTTAGGACCAAGATCCCGAAGGACGCGCCAAAGTGCAGACAAAG 1952

Db 618 CAAGAGGAAGCTTAGGACCAAGATCCCGAAGGACGCGCCAAAGTGCAGACAAAG 559

QY 1953 TGTGAGAGTCTTCCCTGGCTGGAGCACACACAGCTGGCAGAGAGGAGGATGAG 2012

Db 558 TGTGAGAGTCTTCCCTGGCTGGAGCACACACAGCTGGCAGAGAGGAGGATGAG 499

QY 2013 CATCAGAGAGGAGCTGGAGCAAAATGTCGCCCATCTTCTCCAGGCTCTATGGGGG 2072

Db 498 CATCAGAGAGGAGCTGGAGCAAAATGTCGCCCATCTTCTCCAGGCTCTATGGGGG 439

QY 2073 CTTGGTCTCTGGGGGCGAGTGTAGCGCTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 2132

Db 438 CTTGGTCTCTGGGGGCGAGTGTAGCGCTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 379

QY 2133 GSCCCCATCATTTAGGAGGTTGATTTGAATGGCCCTTCTGATAGTCAAGTCAAGTCAAGT 2192

Db 378 GSCCCCATCATTTAGGAGGTTGATTTGAATGGCCCTTCTGATAGTCAAGTCAAGTCAAGT 319

QY 2193 AGGGCTATGCTATGGCCCTTCTAGACTCTTCTATGATCTCTGCTTCTGATAGTCAAGTCAAGT 2252

Db 318 AGGGCTATGCTATGGCCCTTCTAGACTCTTCTATGATCTCTGCTTCTGATAGTCAAGTCAAGT 259

QY 2253 GCTTGGGGGGGCTTCCCTCCAAAGCTAGAACTTCTTCCAGGATCAAGTCAAGTCTTTT 2312

Db 258 GCTTGGGGGGGCTTCCCTCCAAAGCTAGAACTTCTTCCAGGATCAAGTCAAGTCTTTT 199

QY 2313 GACTTTTGGGGGGGCGGTTTCATCTCTTCTGCTTCTGCTTCAATATAAAGTCAATTAATTA 2372

Db 198 GACTTTTGGGGGGGCGGTTTCATCTCTTCTGCTTCTGCTTCAATATAAAGTCAATTAATTA 139

QY 2373 TTAATACTTGTGTGGCACTTTAAACATGCTTCACTATATTTTCTGTATTTTGTACTT 2432

Db 138 TTAATACTTGTGTGGCACTTTAAACATGCTTCACTATATTTTCTGTATTTTGTACTT 79

QY 2433 GTATGATGAATTTTGTATGATAAATAATAGTTATAGACTTAATAAATCTTTTAAACTC 2492

Db 78 GTATGATGAATTTTGTATGATAAATAATAGTTATAGACTTAATAAATCTTTTAAACTC 19

RESULT 2

BU617655/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BU617655 707 bp mRNA linear EST 23-SEP-2002

UI-H-DF0-beq-b-22-0-UI-e1 NCI CGAP DF0 Homo sapiens cDNA clone

UI-H-DF0-beq-b-22-0-UI 3', mRNA sequence.

BU617655

BU617655.1 GI:23283870

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 707)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Dr. Jose Marcuende

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYA=yes.

Location/Qualifiers

1..707

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-DF0-beq-b-22-0-UI"

/tissue_type="Subchondral Bone"

/lab_host="PH10B (Life Technologies)"

/clone_lib="NCI-CGAP_DF0"

/notes="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.

TAG_LIB=UI-H-DF0

TAG_SEQ=GTTAAGCGTC"

ORIGIN

Query Match 26.4%; Score 659; DB 3; Length 707;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1834 ACAGAGTGGTCCAAAACCTCGCTGGAGGCCATGCTTCCATGTGAAGTCTTTTG 1893

Db 677 ACAGAGTGGTCCAAAACCTCGCTGGAGGCCATGCTTCCATGTGAAGTCTTTTG 618

QY 1894 AAGAGGAAGCTTAGGAGCAAGATTCGGAAGGACAGCGGCAAGTGCAGACAAGT 1953

Db 617 AAGAGGAAGCTTAGGAGCAAGATTCGGAAGGACAGCGGCAAGTGCAGACAAGT 558

QY 1954 GTCAGAGTCTTCTGCTGGAGCAACACAGCTGGCAGAGAGGAGGATGTAGC 2013

Db 557 GTCAGAGTCTTCTGCTGGAGCAACACAGCTGGCAGAGAGGAGGATGTAGC 498

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Qy 2014 ATCAGAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCAGGCTCTATGGGGGC 2073
Db 497 ATCAGAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCAGGCTCTATGGGGGC 438
Qy 2074 CTGGTGTCCTGGGGGAGCAGTGTAGCGCTCAGCGCCACCGAGGGGAGCCAGCACCG 2133
Db 437 CTGGTGTCCTGGGGGAGCAGTGTAGCGCTCAGCGCTCAGCGCCACCGAGGGGAGCCAGCACCG 378
Qy 2134 GCCCATCATTTAGGAGGTTGATTGAATGGCCCTCTGTGATAGTCAAGTCAAGTCTGACTGTCA 2193
Db 377 GCCCATCATTTAGGAGGTTGATTGAATGGCCCTCTGTGATAGTCAAGTCTGACTGTCA 318
Qy 2194 GGGCTATGCTATGGCCCTTCTAGACTCTCTTATGATCTCTGCTTCCCTTCAGAGTGAAGGG 2253
Db 317 GGGCTATGCTATGGCCCTTCTAGACTCTCTTATGATCTCTGCTTCCCTTCAGAGTGAAGGG 258
Qy 2254 CTGGGGGGCTCTCCCTCCAAAGCTAGAACTTCTTCCAGTAACTGAACTCTTTG 2313
Db 257 CTGGGGGGGCTCTCCCTCCAAAGCTAGAACTTCTTCCAGTAACTGAACTCTTTG 198
Qy 2314 ACTTTTGGGGGAGGCGGTTCACTCTCTCTGCTTCAATATAAAAGTCAATTAATTAT 2373
Db 197 ACTTTTGGGGGAGGCGGTTCACTCTCTCTGCTTCAATATAAAAGTCAATTAATTAT 138
Qy 2374 TAAACTTGTGTGGCACTTTAAACATTTTCACTTACCTATATTTTGTGTAATTTGTTACTTG 2433
Db 137 TAAACTTGTGTGGCACTTTAAACATTTTCACTTACCTATATTTTGTGTAATTTGTTACTTG 78
Qy 2434 TATGTAGTAATTTTGTATGTAATAATAGTATAGACCTTAATAACTTTTAAACTC 2492
Db 77 TATGTAGTAATTTTGTATGTAATAATAGTATAGACCTTAATAACTTTTAAACTC 19
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RESULT 3

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BO918107
LOCUS BO918107
DEFINITION AGENCOURT 8822790 Lupski_sciatic_nerve mRNA linear EST 20-AUG-2002
IMAGE:6203181 5', mRNA sequence.
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BO918107

BO918107.1 GI:22332805

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo;

1 (bases 1 to 936)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LUMI3622 row: g column: 22

High quality sequence stop: 650.

Location/Qualifiers

1. .936

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6203181"

/sex="male"

/tissue_type="sciatic nerve"

/dev_stage="adult, 70 yr"

/lab_host="DH10B"

/clone_lib="Lupski_sciatic_nerve"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCAGGCTCCG-3' and
5'-GACTAGTTCTAGATCCGAGCGGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupeki, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

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Query Match 25.4%; Score 632; DB 3; Length 936;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1136 GCCCGCTTTGAGGAACCTGTCTCAGACCTTCTCCGAGACACCTTGAGCGGTGGAGAAG 1195  
Db 1 GCCCGCTTTGAGGAACCTGTCTCAGACCTTCTCCGAGACACCTTGAGCGGTGGAGAAG 60  
  
Qy 1196 GCCCTCGGGGATGCCAAGCTGGACAAAGGCCAGATTTCATGACTTCTTCAACGGCAAGAGCT 1255  
Db 61 GCCCTCGGGGATGCCAAGCTGGACAAAGGCCAGATTTCATGACTTCTTCAACGGCAAGAGCT 120  
  
Qy 1256 CTCACCTCGCATCCCCAAGGTGACAAAGTTGCTGCAAGGACTTCTTCAACGGCAAGAGCT 1315  
Db 121 CTCACCTCGCATCCCCAAGGTGACAAAGTTGCTGCAAGGACTTCTTCAACGGCAAGAGCT 180  
  
Qy 1316 GAACAAGACATCAACCTCTGATGAGCTGTGGCTTATGGGTCTGTCTGACGCGGCCGT 1375  
Db 181 GAACAAGACATCAACCTCTGATGAGCTGTGGCTTATGGGGCTGTCTGACGCGGCCGT 240  
  
Qy 1376 GTTGATGGGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGCTGCGAGTGCCTCCCT 1435  
Db 241 GTTGATGGGGGACAAATGTGAGAAAGTGCAGGATCTCTGCTGCTGCGAGTGCCTCCCT 300  
  
Qy 1436 GTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGACACCGCTGATCCAGAGGAACGCCAC 1495  
Db 301 GTCTCTGGGGCTGGAGACAGCAGGTGGGTGATGACACCGCTGATCCAGAGGAACGCCAC 360  
  
Qy 1496 TATCCCCACCAAGCAGACCCAGATTTCACACCTTCTGCGACCAACAGCTGGGGTCTT 1555  
Db 361 TATCCCCACCAAGCAGACCCAGATTTCACACCTTCTGCGACCAACAGCTGGGGTCTT 420  
  
Qy 1556 CATCCAGGTGATGAGTTGAGAGGCCATGACCAAGGACCAACCTCTCGGGGGT 1615  
Db 421 CATCCAGGTGATGAGTTGAGAGGCCATGACCAAGGACCAACCTCTCGGGGGT 480  
  
Qy 1616 TGAACCTCATTTGGCATCCCTCTGCCCCACATGGAGTCCCCCAGATAGAGTGCATTTGA 1675  
Db 481 TGAACCTCATTTGGCATCCCTCTGCCCCACATGGAGTCCCCCAGATAGAGTGCATTTGA 540  
  
Qy 1676 CATTTATGCTAATGGCATCTCTGAGCGTGCAGCCACTGACAGGACACAGGTAAGCTAA 1735  
Db 541 CATTTATGCTAATGGCATCTCTGAGCGTGCACAGCCACTGACAGGACACAGGTAAGCTAA 600  
  
Qy 1736 CAAGATCACAATGACAGGGCCGCTGACAGAGGAGGAGGAGGAGGAGTGTTCATCA 1795  
Db 601 CAAGATCACAATGACAGGGCCGCTGACAGAGGAGGAGGAGGAGGAGTGTTCATCA 660  
  
Qy 1796 AGCCGAGCAGTACGGGGCTGAGGATGAGGCCACAGAGGACAGAGTGGTGCACAAAATC 1855  
Db 661 AGCCGAGCAGTACGGGGCTGAGGATGAGGCCACAGAGGACAGAGTGGTGCACAAAATC 720  
  
Qy 1856 GCTGAGGCCCATG 1869  
Db 721 GCTGAGGCCCATG 734
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RESULT 4

DR004990

LOCUS

DEFINITION

TC118784 Human placenta, large insert, pCMV expression library Homo

sapiens

EST 17-MAY-2005

linear

mRNA

709 bp

pCMV expression library Homo

D0
D1
D2
D3
D4
D5
D6
D7
D8
D9
DA
DB
DC
DD
DE
DF
E0
E1
E2
E3
E4
E5
E6
E7
E8
E9
EA
EB
EC
ED
EE
EF
F0
F1
F2
F3
F4
F5
F6
F7
F8
F9
FA
FB
FC
FD
FE
FF

100 CCGGCTGGAGATCCTTGTGCCAACGACCAAGGGCAACGCACCACGCCCACT 359

300 TTCAGCAGGGCCGCTGGAGATCCTTGTGCCAACGACCAAGGGCAACGCACCACGCCCACT 359

the normalized library NCI_CGAP Lu5 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "		Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jose Mercuende CDNA Library prepared by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu Seq primer: M13 FORWARD POLYA=Yes.	
ORIGIN		FEATURES	
Query Match Best Local Similarity 100.0%; Pred. No. 5.6e-300; Length 698; Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Location/Qualifiers 1..676 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-DF0-bek-o-20-0-UI" /tissue_type="Subchondral Bone" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI CGAP DF0" /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dtr)18 tail. The sequence tag for this library is GTTAAGCGTC. TAG_L1B=UI-H-DF0 TAG_L1B=UI-H-DF0 TAG_SEQ=GTTAAGCGTC"	
1906	TTAGGACAAGATTCCGAGAGGACAGGGCGCAAGTGCAAGCAAACTGTGAGGAAGTCC 1965	QY	
591	TTAGGACAAGATTCCGAGAGGACAGGGCGCAAGTGCAAGCAAACTGTGAGGAAGTCC 532	Db	
1966	TTGGCTGGCTGGAGCACACAGCTGGCAGAGAGGAGGATGAGCATCAGAAGAGGG 2025	QY	
531	TTGGCTGGCTGGAGCACACAGCTGGCAGAGAGGAGGATGAGCATCAGAAGAGGG 472	Db	
2026	AGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTGTGTCCTCG 2085	QY	
471	AGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTGTGTCCTCG 412	Db	
2086	GGGGACAGAGTTGTAGCGCTCAAGCCACAGGGGGACCCAGCACCGGCGCCCATCATTTG 2145	QY	
411	GGGGACAGAGTTGTAGCGCTCAAGCCACAGGGGGACCCAGCACCGGCGCCCATCATTTG 352	Db	
2146	AGGAGGTTGATGAATGGCCCTTCGTGATAAGTCAGCTGTGACTGTGAGGGCTATGCTAT 2205	QY	
351	AGGAGGTTGATGAATGGCCCTTCGTGATAAGTCAGCTGTGACTGTGAGGGCTATGCTAT 292	Db	
2206	GGGCTTCTAGACTGTCTTATGATCCTGCCTTCAGAGATGAAGGCTTGGGGGGTCC 2265	QY	
291	GGGCTTCTAGACTGTCTTATGATCCTGCCTTCAGAGATGAAGGCTTGGGGGGTCC 232	Db	
2266	TTCCCTCCAAAGCTAGAACTTCTTCCAGGATAAAGTGAAGTCTTTTGAATTTTGGGGG 2325	QY	
231	TTCCCTCCAAAGCTAGAACTTCTTCCAGGATAAAGTGAAGTCTTTTGAATTTTGGGGG 172	Db	
2326	GAGGGGGTTCATCTCTTCTGCTTCAATAAAGTCATTAATTTATTAAGTCTGTGT 2385	QY	
171	GAGGGGGTTCATCTCTTCTGCTTCAATAAAGTCATTAATTTATTAAGTCTGTGT 112	Db	
2386	GGCACTTTAACTGCTTTCACCTATATTTTGTGATTTTGTACTTGTATGATGAATT 2445	QY	
111	GGCACTTTAACTGCTTTCACCTATATTTTGTGATTTTGTACTTGTATGATGAATT 52	Db	
2446	TTGTTATGTAATAATATAGTTATAGACCTAAATAAATTTTAAACTC 2492	QY	
51	TTGTTATGTAATAATATAGTTATAGACCTAAATAAATTTTAAACTC 5	Db	
RESULT 6 CA426117/c LOCUS DEFINITION UI-H-DF0-bek-o-20-0-UI.s1 NCI_CGAP_DF0 Homo sapiens cDNA clone UI-H-DF0-bek-o-20-0-UI 3', mRNA sequence. CA426117 ACCESSION VERSION KEYWORDS SOURCE CA426117.1 GI:24788843 EST. Homo sapiens (human) Homo sapiens ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 676) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. AUTHORS TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index JOURNAL Unpublished (1997) COMMENT Contact: Robert Strausberg, Ph.D.			
1911	GACAAGATTCCGAGAGGACAGGGCGCAAGTGCAAGCAAACTGTGAGGAAGTCTTGGC 1970	QY	
600	GACAAGATTCCGAGAGGACAGGGCGCAAGTGCAAGCAAACTGTGAGGAAGTCTTGGC 541	Db	
1971	TGGCTGGAGCACAAACAGCTGCGAGAGAGGAGGATGAGCATCAGAAGAGGAGCTG 2030	QY	
540	TGGCTGGAGCACAAACAGCTGCGAGAGAGGAGGAGTATGAGCATCAGAAGAGGAGCTG 481	Db	
2031	GAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTGTGCTCCCTGGGGGC 2090	QY	
480	GAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTGTGCTCCCTGGGGGC 421	Db	
2091	AGCAGTTGTAGCGCTCAAGCCACAGGGGGAGCCAGCACCGGCGCCCATCATTTGAGGAG 2150	QY	
420	AGCAGTTGTAGCGCTCAAGCCACAGGGGGAGCCAGCACCGGCGCCCATCATTTGAGGAG 361	Db	
2151	GTTGATTGAATGGCCCTTCGTGATAAGTCAGCTGTGACTGTGAGGGCTATGCTATGGGCC 2210	QY	
360	GTTGATTGAATGGCCCTTCGTGATAAGTCAGCTGTGACTGTGAGGGCTATGCTATGGGCC 301	Db	
2211	TTCTAGACTGTCTTCTATGATCCTCCCTTCAGAGATGAAGGCTTGGGGGGTCTTCCC 2270	QY	
300	TTCTAGACTGTCTTCTATGATCCTCCCTTCAGAGATGAAGGCTTGGGGGGTCTTCCC 241	Db	
2271	TCCAAAGCTAGAACTTCTTTCCAGGATAAAGTGAAGTCTTTTGACTTTTGGGGGGAGGG 2330	QY	
240	TCCAAAGCTAGAACTTCTTTCCAGGATAAAGTGAAGTCTTTTGACTTTTGGGGGGAGGG 181	Db	
2331	CGGTTATCTCTTCTGCTTCAAAATAAAGTCATTAATTTATTAAGTCTTGTGGGCAC 2390	QY	
180	CGGTTATCTCTTCTGCTTCAAAATAAAGTCATTAATTTATTAAGTCTTGTGGGCAC 121	Db	

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QY 2391 TTTAACAATGCTTTACCTATATTTTGTGTATTTTGTACTTGTATGATGAATTTTGT 2450
Db 120 TTTAACAATGCTTTACCTATATTTTGTGTATTTTGTACTTGTATGATGAATTTTGT 61
QY 2451 ATGTAAATATAGTTATAGACCTTAATAAATTAACCTTTTAAATC 2492
Db 60 ATGTAAATATAGTTATAGACCTTAATAAATTAACCTTTTAAATC 19

RESULT 7
CA391777 579 bp mRNA linear EST 06-NOV-2002
LOCUS csl8905.y1 Human Retinal pigment epithelium/choroid cDNA
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone csl8905
5', mRNA sequence.
ACCESSION CA391777
VERSION CA391777.1 GI:24723954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 579)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human RPE/choroid for the
NEIbank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
12107410
JOURNAL PUBLISHED
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 18 row: g column: 05
Seq primer: M13Rp1 reverse primer (ABI).
Location/Qualifiers
1. .579
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"
/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>. The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."
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ORIGIN

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Query Match 23.2%; Score 579; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 9.9e-296;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 690 GTAACTCGCAGCGCCAGCCACCAAGGACGCGGGGGCCATCGCGGGCTCAAGGTGTGC 749
Db 1 GTAACTCGCAGCGCCAGCCACCAAGGACGCGGGGGCCATCGCGGGCTCAAGGTGTGC 60
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QY 750 CGATCATCAATGAGCCACGCGCAGAGCCATCGCTATGGGCTGAGCCGGCGGCGCG 809
Db 61 CGATCATCAATGAGCCACGCGCAGAGCCATCGCTATGGGCTGAGCCGGCGGCGCG 120
QY 810 GAAAGCGCAACGTGCTCATTTTGTACCTGGGTGGGGGCACTTCGATGTGCGTTCTCT 869
Db 121 GAAAGCGCAACGTGCTCATTTTGTACCTGGGTGGGGGCACTTCGATGTGCGTTCTCT 180
QY 870 CCATTGACCGCGGTGTCTTTGAGGTGAAAGCCACCTGCTGGAGATACCCACCTGGGAGGAG 929
Db 181 CCATTGACCGCGGTGTCTTTGAGGTGAAAGCCACCTGCTGGAGATACCCACCTGGGAGGAG 240
QY 930 AGGACTTCGACACACCGGCTCGTGAACACTTTCATGGAAGAATTCGCGCGGAAGCATGGGA 989
Db 241 AGGACTTCGACACACCGGCTCGTGAACACTTTCATGGAAGAATTCGCGCGGAAGCATGGGA 300
QY 990 AGGACCTGAGCGGGAAACAAGCGTCCCTGCGCAGGCTGGCAGAGCTGTGAGCGCGCCA 1049
Db 301 AGGACCTGAGCGGGAAACAAGCGTCCCTGCGCAGGCTGGCAGAGCTGTGAGCGCGCCA 360
QY 1050 AGCGACCCCGTCTCTCCAGCAGCCAGCCAGCCAGCTGGAGATAGACTCCCTGTTTCGAGGGCG 1109
Db 361 AGCGACCCCGTCTCTCCAGCAGCCAGCCAGCCAGCTGGAGATAGACTCCCTGTTTCGAGGGCG 420
QY 1110 TGGACTTCTACAAGTCCATCACTCTGTCGCCGCTTTGAGGAACCTGTGCTAGACTCTTCC 1169
Db 421 TGGACTTCTACAAGTCCATCACTCTGTCGCCGCTTTGAGGAACCTGTGCTAGACTCTTCC 480
QY 1170 GCAGCACCTGAGCGCGGTGGAGAGCCCTGCGGGATGCCAAGCTGGACAAGGCCCAGA 1229
Db 481 GCAGCACCTGAGCGCGGTGGAGAGCCCTGCGGGATGCCAAGCTGGACAAGGCCCAGA 540
QY 1230 TTCATGACTTCGTCCTGGGGGAGGGCTCCACTCGCATC 1268
Db 541 TTCATGACTTCGTCCTGGGGGAGGGCTCCACTCGCATC 579
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RESULT 8

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BX357704/c 1003 bp mRNA linear EST 08-APR-2004
LOCUS BX357704 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION clone CS0D1029VJ23 3-PRIME, mRNA sequence.
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ACCESSION BX357704
VERSION BX357704.2 GI:46289402
KEYWORDS EST.
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SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1003)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370149.
```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 Evry cedex - FRANCE
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1112.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0D1029CE12NP1&c=1112.f.
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FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

Query Match 22.6%; Score 564; DB 4; Length 1003;
Best Local Similarity 99.4%; Pred. No. 1e-287;
Matches 814; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1599 AACCTGCTGGGCGCTTTTGAACATCATTTGGCATCCTCTGCCCCACATGGAGTCCCCCAG 1658
Db 860 AACCTGCTGGGCGCTTTTGAACATCATTTGGCATCCTCTGCCCCACATGGAGTCCCCCAG 801

Qy 1659 ATAGAGTGACGTTTGACATGATGCTAATGGCATCTGAGCGTGACAGCACTGACAGG 1718
Db 800 ATAGAGTGACGTTTGACATGATGCTAATGGCATCTGAGCGTGACAGCACTGACAGG 741

Qy 1719 AGCACAGTGAAGGCTAACAGATCACCAATGACAAAGGCGCGCTGACAAAGGAGGAGTG 1778
Db 740 AGCACAGTGAAGGCTAACAGATCACCAATGACAAAGGCGCGCTGACAAAGGAGGAGTG 681

Qy 1779 GAGAGGATGTTTCATGAAGCGGACGATACCGGGCTGAGGATGAGGCCCCAGAGGGACAGA 1838
Db 680 GAGAGGATGTTTCATGAAGCGGACGATACCGGGCTGAGGATGAGGCCCCAGAGGGACAGA 621

Qy 1839 GTGGCTGCCAAAACCTCGTGGAGGCCCATGTCTTCATGTGAAGTTCTTTGCAAGAG 1898
Db 620 GTGGCTGCCAAAACCTCGTGGAGGCCCATGTCTTCATGTGAAGTTCTTTGCAAGAG 561

Qy 1899 GAAAGCCTTAGGGACAGATTTCCGAGAGAGACAGAGCGCAAGTGCAGACAAAGTGTGAC 1958
Db 560 GAAAGCCTTAGGGACAGATTTCCGAGAGAGACAGAGCGCAAGTGCAGACAAAGTGTGAC 501

Qy 1959 GAAGTCCTTGCTGGCTGGAGCAACAACAGCTGGCAGAGAGGAGGATGATGAGCATCAG 2018
Db 500 GAAGTCCTTGCTGGCTGGAGCAACAACAGCTGGCAGAGAGGAGGATGATGAGCATCAG 441

Qy 2019 AAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGGCTGTGT 2078
Db 440 AAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGGCTGTGT 381

Qy 2079 GTCCCTGGGGGACAGCAGTTGTAGCGCTCAAGCGCCACCCAGGGGACCCAGACACCGGCCCC 2138
Db 380 GTCCCTGGGGGACAGCAGTTGTAGCGCTCAAGCGCCACCCAGGGGACCCAGACACCGGCCCC 321

Qy 2139 ATCAATTGAGGAGGTTGATTTGAATGGCCCTTTCGTGATAAGTCAGCTGTGACGCTGTCAGGGCT 2198
Db 320 ATCAATTGAGGAGGTTGATTTGAATGGCCCTTTCGTGATAAGTCAGCTGTGACGCTGTCAGGGCT 261

Qy 2199 ATGCTATGGGCTTCTAGACTGTCTTCTATGATGCTTGCCTTCAGAGATGAAGGCTGTG 2258
Db 260 ATGCTATGGGCTTCTAGACTGTCTTCTATGATGCTTGCCTTCAGAGATGAAGGCTGTG 201

Qy 2259 GGGGGTCTTCCCTCCAAAGCTAGAACTTCTTCTCCAGGATACTGAAGTCTTTTGACTTT 2318
Db 200 GGGGGTCTTCCCTCCAAAGCTAGAACTTCTTCTCCAGGATACTGAAGTCTTTTGACTTT 141

Qy 2319 TTGGGGGAGGGGGGTTTCATCTCTTCTGCTTCAAAATAAAAGTCATTAATTTATTAATA 2378
Db 140 TTGGGGGAGGGGGGTTTCATCTCTTCTGCTTCAAAATAAAAGTCATTAATTTATTAATA 81

Qy 2379 CTTGTGTGGCACTTTAACTGCTTTTCACTATATTTT 2417
Db 80 CTTGTGTGGCACTTTAACTGCTTTTCACTATATTTT 42

RESULT 9
AI652340/c
LOCUS

DEFINITION
wb60d02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2310051 3', similar to gb:X51757_cds1 HEAT SHOCK 70 KD PROTEIN 6 (HUMAN);, mRNA sequence.

ACCESSION
AI652340
VERSION
AI652340.1 GI:4736319
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 537)
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 625 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 471.
Location/Qualifiers
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/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIdb 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:2310051"
/tissue type="pooled germ cell tumors"
/lab_host="DH10B"
/clone lib="NCI CGAP GC6"
/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIdb 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 21.5%; Score 535; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.6e-272;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1958 GGAAGTCTCTGCTGGCTGGAGCAACACAGCTGGCAGAGAGGAGGATGATGAGCATCA 2017
Db 537 GGAAGTCTCTGCTGGCTGGAGCAACACAGCTGGCAGAGAGGAGGATGATGAGCATCA 478

Qy 2018 GAAGAGGAGCTGGAGCAAAATCTGCGCCCATCTTCTCAGGCTCTATGGGGGGCTGG 2077
Db 477 GAAGAGGAGCTGGAGCAAAATCTGCGCCCATCTTCTCAGGCTCTATGGGGGGCTGG 418

Qy 2078 TGTCCCTGGGGGACGAGTTGTAGCGCTCAAGCCACAGGGGGACCCAGACACCGGCCC 2137
Db 417 TGTCCCTGGGGGACGAGTTGTAGCGCTCAAGCCACAGGGGGACCCAGACACCGGCCC 358

Qy 2138 CATCATTTGAGGAGGTTGATTTGAATGGCCCTTCGTGATAAGTCAGCTGTGACGCGC 2197
Db 357 CATCATTTGAGGAGGTTGATTTGAATGGCCCTTCGTGATAAGTCAGCTGTGACGCGC 298

Qy 2198 TATGCTATGGGCTTCTAGACTGTCTTCTATGATCTCTGCCCCTTCAGAGATGAAGGCTTG 2257
Db 297 TATGCTATGGGCTTCTAGACTGTCTTCTATGATCTCTGCCCCTTCAGAGATGAAGGCTTG 238

us-10-764-316-7.olig.rst

Mon Nov 6 11:55:56 2006

Qy	1839	GTGGCTGCCAAAACCTCGCTGGAGGCCCATGTCTTCCATGTGAAAGTCTTTTGCAGAG	1898
Db	534	GTGGCTGCCAAAACCTCGCTGGAGGCCCATGTCTTCCATGTGAAAGTCTTTTGCAGAG	475
Qy	1899	GAAAGCCTTAGGACCAAGATTCCCGAAGGACAGCGGCAAGTGAACAAGTCTCAG	1958
Db	474	GAAAGCCTTAGGACCAAGATTCCCGAAGGACAGCGGCAAGTGAACAAGTCTCAG	415
Qy	1959	GAATCTCTGCTGGTGGAGCAACCCAGCTGCAGAGAGGAGGATGAGCATCAG	2018
Db	414	GAATCTCTGCTGGTGGAGCAACCCAGCTGCAGAGAGGAGGATGAGCATCAG	355
Qy	2019	AAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTTGGT	2078
Db	354	AAGAGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCCAGGCTCTATGGGGGCTTGGT	295
Qy	2079	GTCCCTGGGGGACAGCTTGTAGGCTCAAGCCACAGCGGGGACCCAGCACCGGCCCC	2138
Db	294	GTCCCTGGGGGACAGCTTGTAGGCTCAAGCCACAGCGGGGACCCAGCACCGGCCCC	235
Qy	2139	ATCATTTGAGGAGTGTGATTAATGCGCTTCGTGATAAGTCAGCTGTGACTGTGAGGCT	2198
Db	234	ATCATTTGAGGAGTGTGATTAATGCGCTTCGTGATAAGTCAGCTGTGACTGTGAGGCT	175
Qy	2199	ATGCTATGGGCTTCTAGACCTGTCTTATGATCTGCTCCCTTCAGAGATGAAGGCTTGG	2258
Db	174	ATGCTATGGGCTTCTAGACCTGTCTTATGATCTGCTCCCTTCAGAGATGAAGGCTTGG	115
Qy	2259	GGGGTCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGCTTTTGTACTT	2318
Db	114	GGGGTCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGCTTTTGTACTT	55
Qy	2319	TTGGGGGAGGGCGGTTCATCTCTTCTGCTTCAATTAATAAGTCAATTAATTA	2372
Db	54	TTGGGGGAGGGCGGTTCATCTCTTCTGCTTCAATTAATAAGTCAATTAATTA	1
RESULT 11			
DB017526			
LOCUS	DB017526	TESOP2 Homo sapiens cDNA clone	linear EST 13-NOV-2005
DEFINITION	DB017526	sequence.	567 bp mRNA
ACCESSION	DB017526	GI:82361027	
VERSION	DB017526.1		
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.	
REFERENCE		1 (bases 1 to 567)	
AUTHORS		Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.	
TITLE		Identification of Transcriptional Modulation: Large-scale Promoters of Human Genes	
JOURNAL		Genome Res. 16 (1), 55-65 (2006)	
PUBMED		16344560	
COMMENT		Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology	

Qy	2258	GGGGGTCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGTCTTTGACTT	2317
Db	237	GGGGGTCTTCCCTCCAAAGCTAGAACTTTCTTCCAGGATAACTGAAGTCTTTGACTT	178
Qy	2318	TTTGGGGGAGGGGTTCACTCTCTTCTGCTTCAATTAATAAGTCAATTAATAA	2377
Db	177	TTTGGGGGAGGGGTTCACTCTCTTCTGCTTCAATTAATAAGTCAATTAATAA	118
Qy	2378	ACTTGTGTGGACCTTTAACTGCTTTACCTAATTTTGTGTAATTTGTTACTTGTATG	2437
Db	117	ACTTGTGTGGACCTTTAACTGCTTTACCTAATTTTGTGTAATTTGTTACTTGTATG	58
Qy	2438	TATGAATTTTGTATGTAATTAATAGTTATAGACCTTAATAACTTTTAAACTC	2492
Db	57	TATGAATTTTGTATGTAATTAATAGTTATAGACCTTAATAACTTTTAAACTC	3

RESULT 10			
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LOCUS	BF590626	534 bp mRNA	linear EST 12-DEC-2000
DEFINITION	7h40h11.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:3318501 3'		
	similar to SW:HS76_HUMAN P17066 HEAT SHOCK 70 KD PROTEIN 6 ; mRNA		
ACCESSION	BF590626		
VERSION	BF590626.1	GI:11683037	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.	
REFERENCE		1 (bases 1 to 534)	
AUTHORS		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL		Unpublished (1997)	
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Cloning: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gbco High quality sequence stop: 474.	

FEATURES			
source			
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3318501"		
	/tissue="colon tumor, RER+"		
	/lab_host="DH10B"		
	/clone_lib="NCI CGAP Col6"		
	/note="Organ: colon; Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Col6 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneID# 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo."		

ORIGIN			
Query Match	21.4%	Score 534; DB 7; Length 534;	
Best Local Similarity	100.0%;	Pred. No. 8.8e-272;	
Matches 534; Conservative	0; Mismatches	0; Indels	0; Gaps

Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

Location/Qualifiers
1..567
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TESOP2007084"
/tissue_type="esophageal, tumor tissue"
/clone_lib="TESOP2"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 20.5%; Score 512; DB 9; Length 567;
Best Local Similarity 99.8%; Pred. No. 4.6e-260;
Matches 562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

114 AGATCCGAGCGGCTGGCGGACAGAAACCGCAGGAGAGCTCACTGTGAGCGCCC 173
Db |||||
5 AGATCCGAGCGGCTGGCGGACAGAAACCGCAGGAGAGCTCACTGTGAGCGCCC 64
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174 TCGACGGCGGACGGCAGCAGCTCCGTGGCTCCAGATCCGACAAAGAGCTTCAGCCA 233
Db |||||
65 TCGACGGCGGAGCGGAGAGCTCCGTGGCTCCAGATCCGACAAAGAGCTTCAGCCA 124
|||
234 TCGAGGCCCCACGGGAGCTCGCGTGGGCATCGACCTGGGCACCACCTACTCTGCGTGG 293
Db |||||
125 TCGAGGCCCCACGGGAGCTCGCGTGGGCATCGACCTGGGCACCACCTACTCTGCGTGG 184
|||
294 GCGTGTTCAGCAGGCGGCGTGAGATCTGGCCAAAGCAGCAGGCGCAACCGCACACGC 353
Db |||||
185 GCGTGTTCAGCAGGCGGCGTGAGATCTGGCCAAAGCAGCAGGCGCAACCGCACACGC 244
|||
354 CCAGCTACGTGGCTTCACGACACCGAGCGGCTGTCGGGAGCGCGGCCCAAGAGCCAGG 413
Db |||||
245 CCAGCTACGTGGCTTCACGACACCGAGCGGCTGTCGGGAGCGCGGCCCAAGAGCCAGG 304
|||
414 CGGCCCTGAACCCCCCAACACCGTGTTCGATGCAAGCGGCTGATCGGGCGCAAGTTTCG 473
Db |||||
305 CGGCCCTGAACCCCCCAACACCGTGTTCGATGCAAGCGGCTGATCGGGCGCAAGTTTCG 364
|||
474 CGGACACACCGTTCAGTCGACATGAGACATGGCCCTTCAGAGTGGTGAAGCGGCG 533
Db |||||
365 CGGACACACCGTTCAGTCGACATGAGACATGGCCCTTCAGAGTGGTGAAGCGGCG 424
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534 GCAAGCCCAAGGTGCGGTATGCTACCGCGGAGGACAGAGCTTCTACCCCGAGGAGA 593
Db |||||
425 GCAAGCCCAAGGTGCGGTATGCTACCGCGGAGGAGACAGAGCTTCTACCCCGAGGAGA 484
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594 TCTCGTCCATGCTGAGCAAGATGAAGAGAGCGCGGAGGCGGTACCTGGGCGAGCCCG 653
Db |||||
485 TCTCGTCCATGCTGAGCAAGATGAAGAGAGCGCGGAGGCGGTACCTGGGCGAGCCCG 544
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654 TGAAGCAGCGATGATCACCCTG 676
Db |||||
545 TGAAGCAGCGATGATCACCCTG 567

RESULT 12

DA828714

LOCUS DA828714 PLACE1 Homo sapiens cDNA clone PLACE1001595 5', mRNA
DEFINITION sequence.

ACCESSION

DA828714

VERSION

DA828714.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1. (bases 1 to 662)

REFERENCE

AUTHORS

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
HRI.

FEATURES

source

Location/Qualifiers
1..662
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1001595"
/tissue_type="placenta"
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/note="Vector: pME18SFL3"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.2e-258;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

458 ATCGGGCGCAAGTTGCGGACACACCGTGCGAGTCGGACATCAAGCACTGGCCCTTCCAG 517
Db |||||
1 ATCGGGCGCAAGTTGCGGACACACCGTGCGAGTCGGACATGAAGCACTGGCCCTTCCAG 60
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518 GTGGTGAGCGAGGCGGCAAGCCCAAGGTGCGGTATGCTACCGGGGAGGACAGCG 577
Db |||||
61 GTGGTGAGCGAGGCGGCAAGCCCAAGGTGCGGTATGCTACCGGGGAGGACAGCG 120
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578 TTCTACCCCGAGAGATCTCGTCCATGCTGAGCAAGATCAAGGAGACGCGCGGCG 637
Db |||||
121 TTCTACCCCGAGAGATCTCGTCCATGCTGAGCAAGATCAAGGAGACGCGCGGCG 180
|||
638 TACCTGGGCGAGCCCGTGGAAGCACGCGATGATCACCGTCCCACTATTTCAGTAACTCG 697
Db |||||
181 TACCTGGGCGAGCCCGTGGAAGCACGCGATGATCACCGTCCCACTATTTCAGTAACTCG 240
|||
698 CAGCGCAGGCGCACCAAGGACCGGGGCGCATCGGGGGCTCAAGGTGTCGCGATCATC 757
Db |||||
241 CAGCGCAGGCGCACCAAGGACCGGGGCGCATCGGGGGCTCAAGGTGTCGCGATCATC 300
|||
758 AATGAGGCCACGCGAGCGCATCCCTATGGGCTGGACCGGGGCGCGGGGAAGCGC 817
Db |||||
301 AATGAGGCCACGCGAGCGCATCCCTATGGGCTGGACCGGGGCGCGGGGAAGCGC 360
|||
818 AACGTGCTCATTTTTGACCTGGGTGGGGCACCTTCGATGTGCTGCTCTCTCAATTGAC 877
Db |||||
361 AACGTGCTCATTTTTGACCTGGGTGGGGCACCTTCGATGTGCTGCTCTCTCAATTGAC 420
|||
878 GCCGTGTCTTTGAGGTGAAGCCCACTGCTGAGATACCCACTGGGAGGAGGACTTTC 937
Db |||||
421 GCCGTGTCTTTGAGGTGAAGCCCACTGCTGAGATACCCACTGGGAGGAGGACTTTC 480
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938 GACACCGGCTCGTCAACCACTTCATGG 965
Db |||||
481 GACACCGGCTCGTCAACCACTTCATGG 508

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RESULT 13
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LOCUS
DEFINITION BQ212261 852 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7675912 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6095753
5', mRNA sequence.
ACCESSION BQ212261
VERSION BQ212261.1 GI:20392319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 852)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13368 row: k column: 18
High quality sequence stop: 589.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:6095753"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/node="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
FEATURES
source
ORIGIN
Query Match 20.2%; Score 503; DB 3; Length 852;
Best Local Similarity 99.8%; Pred. No. 2.9e-255;
Matches 553; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 300 TTCAGCAGGGCCGCTGGAGATCCTGGCCAAACAGCAGGGCAACCGCCACCGCCAGCT 359
DB 1 TTCAGCAGGGCCGCTGGAGATCCTGGCCAAACAGCAGGGCAACCGCCACCGCCAGCT 60
QY 360 ACCTGGCCCTTACCGACACCGAGCGGCTGGTGGGGACCGGCCCAAGAGCCAGGGGCC 419
DB 61 ACCTGGCCCTTACCGACACCGAGCGGCTGGTGGGGACCGGCCCAAGAGCCAGGGGCC 120
QY 420 TGAACCCCAACACACCGTGTTCATGCCAGCGGCTGATCGGGCGCAAGTTCCGGGACA 479
DB 121 TGAACCCCAACACACCGTGTTCATGCCAGCGGCTGATCGGGCGCAAGTTCCGGGACA 180
QY 480 CCACGGTGCAGTCCGACATCAAGCACTGGGCCCTTCCAGGTGGTGGAGCGGGCGGCAAGC 539
DB 181 CCACGGTGCAGTCCGACATCAAGCACTGGGCCCTTCCAGGTGGTGGAGCGGGCGGCAAGC 240
QY 540 CCAAGTGCCTGTATGTACCGGGGAGGACAAAGAGCTTCTACCCCGAGGAGTCTCGT 599
DB 241 CCAAGTGCCTGTATGTACCGGGGAGGACAAAGAGCTTCTACCCCGAGGAGTCTCGT 300
QY 600 CCATGTGTCTGAGCAATCAAGAGACGGCCGAGGCGTACCTGGGCCAGCCCGTGAAGC 659
DB 301 CCATGTGTCTGAGCAATCAAGAGACGGCCGAGGCGTACCTGGGCCAGCCCGTGAAGC 360
QY 660 ACGCAGTGTATACCGTCCCACTTATTTTCAGTAACTCTGCGACCGCCAGCGCCCAAGGAGC 719

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DB 361 ACGCAGTGATCACCGTCCACCTATTTTCAGTAACTCGCAGCGCCAGCCACCAAGGAGC 420
QY 720 CGGGGGCCATCGCGGGGCTCAAGGTGCTCGGATCATCAATGAGGCCACGCGCAGCGCA 779
DB 421 CGGGGGCCATCGCGGGGCTCAAGGTGCTCGGATCATCAATGAGGCCACGCGCAGCGCA 480
QY 780 TGGCTATGGGCTGACCGCGGGCGGGGAAAGCGCAACGCTGCTCATTTTTCACCTGG 839
DB 481 TGGCTATGGGCTGACCGCGGGCGGGGAAAGCGCAACGCTGCTCATTTTTCACCTGG 540
QY 840 GTGGGGGACACCTTC 853
DB 541 GTGGGGGACACCTTC 554

RESULT 14
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LOCUS
DEFINITION A1636649 575 bp mRNA linear EST 14-DEC-1999
ts92b11.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2238717 3'
similar to gb.X51757_cdab1 HEAT SHOCK 70 KD PROTEIN 6 (HUMAN);, mRNA
sequence.
ACCESSION A1636649
VERSION A1636649.1 GI:4687979
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 575)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 616 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
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/node="Vector: p7T3D-Paci; Site 1: Not I; Site 2: Eco RI;
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prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1257096-1258631, 1469084-1470983, and
1475592-1476743). Subtraction by Bento Soares and M.
Fatima Bonaldo."
FEATURES
source
ORIGIN
Query Match 20.0%; Score 499; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 3.8e-253;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db501AGAGAAGGAGGATGATGAGCATCAGAAGAGGAGCTGAGCAAAATCTGTGCGCCCACTTT442

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QY2114CCAGGGGAGCCCAAGCAGCCGCCCATCATTTGAGGAGGTTGATTGAATGGCCCTTCTGTGA2173

Db381CCAGGGGAGCCCAAGCAGCCGCCCATCATTTGAGGAGGTTGATTGAATGGCCCTTCTGTGA322

QY2174TAACTGAGCTGTGACTGTGAGGCTATGCTATGAGGCTTCTAGACTGCTTCTATGATCC2233

Db321TAACTGAGCTGTGACTGTGAGGCTATGCTATGAGGCTTCTAGACTGCTTCTATGATCC262

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Db261TGCCCTTTGAGAGTGAAGGGCTTGCGGGGCTTTCCTCTCCAAAGCTAGAACTTTCTTTCC202

QY2294AGGATAACTGAAGTCTTTTGACTTTTGGGGGAGGGCGGTTCATCTCTTCTGCTTCAA2353

Db201AGGATAACTGAAGTCTTTTGACTTTTGGGGGAGGGCGGTTCATCTCTTCTGCTTCAA142

QY2354ATAAAAGTCAATTAATTTATAAATCTGCTGAGCACTTTAACTTTCACTTATAT2413

Db141ATAAAAGTCAATTAATTTATAAATCTGCTGAGCACTTTAACTTTCACTTATAT82

QY2414TTTGTGTATTTTGTACTGTGATGATGAATTTTGTATGATGAATTTTGTATGAATATATAGTATAGACCT2473

Db81TTTGTGTATTTTGTACTGTGATGATGAATTTTGTATGATGAATTTTGTATGAATATATAGTATAGACCT22

QY2474AAATAAACTTTTAAACTC2492

Db21AAATAAACTTTTAAACTC3

RESULT 15

BX348810

LOCUS

DEFINITIONBX348810 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

ACCESSIONBX348810

VERSIONBX348810.2

KEYWORDSGI:46554426

SOURCEEST.

ORGANISMHomo sapiens (human)

REFERENCE1 (bases 1 to 877)

AUTHORSLi, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLEFull-length cDNA libraries and normalization

JOURNALUnpublished (2001)

COMMENTOn May 5, 2003 this sequence version replaced gi:30383328.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seegref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

1112.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?8=CS0BAG028ZB11_CS02674_1&c=1112.f

FEATURES

source

Location/Qualifiers

1..877

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI029YJ23"

ORIGIN

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Best Local Similarity100.0%; Pred. No. 1.6e-251;

Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY365GCCTTCCAGCAGACACCGAGCGGCTGTGCTCGGGGAGCGCCCAAGAGCCAGCGGCGCTGAAC424

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QY425CCCCAACACCGCTGTTCATGCGCGGCTGATCGGGGCAAGTTCGGGAGCACACACG484

Db111CCCCAACACCGCTGTTCATGCGCGGCTGATCGGGGCAAGTTCGGGAGCACACACG170

QY485GTGCACTCGGAGCATGAAGCACCTGGCCCTTCCAGGTGCTGAGCGAGGGCGGCAAGCCCAAG544

Db171GTGCACTCGGAGCATGAAGCACCTGGCCCTTCCAGGTGCTGAGCGAGGGCGGCAAGCCCAAG230

QY545GTGCGGTATGCTTACCGCGGGGAGGAGCAAGAGAGTTCACCCGAGAGAGATCTCGTCCATG604

Db231GTGCGGTATGCTTACCGCGGGGAGGAGCAAGAGAGTTCACCCGAGAGAGATCTCGTCCATG290

QY605GTGCTGAGCAAGATGAAGAGAGCGCGGCGGTACCTGGGCGAGCCCTGTAAGCAGCA664

Db291GTGCTGAGCAAGATGAAGAGAGCGCGGCGGTACCTGGGCGAGCCCTGTAAGCAGCA350

QY665GTGATCACCGTGCCTTATTTTCACTGTAAGTTCGAGCGCGGCGGCAAGAGCGCGGG724

Db351GTGATCACCGTGCCTTATTTTCACTGTAAGTTCGAGCGCGGCGGCAAGAGCGCGGG410

QY725GCCATCGCGGGGCTCAAGGTGCTGCGGATCATCAATGAGGCCCAAGAGCGAGCATCGCC784

Db411GCCATCGCGGGGCTCAAGGTGCTGCGGATCATCAATGAGGCCCAAGAGCGAGCATCGCC470

QY785TATGGGCTGAGACCGCGGGGCGCGGAAAGCGCAACGTGCTCATTTTTCACCTGGGTGG844

Db471TATGGGCTGAGACCGCGGGGCGCGGAAAGCGCAACGTGCTCATTTTTCACCTGGGTGG530

QY845GGCACCTTCGATGTGT860

Db531GGCACCTTCGATGTGT546

Search completed: November 4, 2006, 01:09:04

Job time: 10968.4 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2493	100.0	2493	5	AF093759	Ar093759 Homo sapi
2	2442	98.0	147060	12	AC021370	AC021370 Homo sapi
3	2442	98.0	150019	2	AL451067	AL451067 Human DNA
4	913	36.6	1914	5	CQ730982	CQ730982 Sequence
5	502	20.1	2279	5	BC035665	BC035665 Homo sapi
6	495	19.9	2318	5	AK223362	AK223362 Homo sapi
7	495	19.9	129505	5	ALU590385	ALU590385 Human DNA
8	484	19.4	2236	2	AR531647	AR531647 Sequence
9	444	17.8	2253	5	AK093925	AK093925 Homo sapi
10	444	17.8	136035	12	BX537284	BX537284 Homo sapi
11	431	17.3	2962	2	AR454599	AR454599 Sequence
12	350	14.0	401	7	BV198650	BV198650 sgmm19841
13	329	13.2	1001	5	S78631	S78631 HSPA6=70-kd
14	328	13.2	2492	2	AK336488	AK336488 Sequence
15	329	13.2	2492	5	HSP70B	X515757 Human heat-
16	259	10.4	1001	2	CQ853748	CQ853748 Sequence
17	236	9.5	401	7	BV193391	BV193391 sgmm17768
18	226	9.1	1180	5	HSP70BG	X51758 Human mRNA

Best Local Similarity 100.0%; Pred. No. 0; Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CCCCGGGGGGGGGGAGGCTCTCGACTGGGCGGGAAGTTCGGGAAGTTTCGGGGG	60						
Db	1	CCCCGGGGGGGGGGAGGCTCTCGACTGGGCGGGAAGTTCGGGAAGTTTCGGGGG	60						
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Qy	301	TCAGCAGGCGCGGTGGAGATCTGGCCAAACGACAGGGCAACCGCAACGCGCCAGCTA	360						
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Db	781	CGCCTATGGGTGAGACCGCGGGGCGGGAAGCGCAACGTCTCATTTTGAACCTGGG	840						
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RESULT 3
AL451067

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DEFINITION	Human DNA sequence from clone RP11-25X21 on chromosome 1, complete sequence.											
ACCESSION	AL451067	AC031995										
VERSION	AL451067.12	GI:62177046										
KEYWORDS	HTG.											
SOURCE	Homo sapiens (human)											
ORGANISM	Homo sapiens											
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.											
REFERENCE	1 (bases 1 to 150019)											
AUTHORS	Barlow, K.											
TITLE	Direct Submission											
JOURNAL	Submitted (02-APR-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk											
COMMENT	On Apr 2, 2005 this sequence version replaced gi:62148838. Draft Sequence Produced by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA http://www-seq.wi.mit.edu ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk											

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

sequence of the clone being a rat. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone configs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP11-25K21 is from the library RPC1-11.1 constructed by the group of Flierle de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6.

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FEATURES
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Db	71239	CA	CG	T	G	CA	GT	CG	GA	AT	CC	AG	CG	CT	G	AT	CC	AG	CG	CG	CG	71298
QY	541	CA	AG	GT	CG	CG	AT	CT	AC	CG	GG	AG	CA	AG	CT	T	AC	CG	GG	AG	CA	600
Db	71299	CA	AG	GT	CG	CG	AT	CT	AC	CG	GG	AG	CA	AG	CT	T	AC	CG	GG	AG	CA	71358
QY	601	CA	TG	T	G	CT	C	AG	AA	GA	AG	AG	AG	CG	CG	AG	CT	T	CG	GG	CG	660
Db	71359	CA	TG	T	G	CT	C	AG	AA	GA	AG	AG	AG	CG	CG	AG	CT	T	CG	GG	CG	71418
QY	661	CG	CA	GT	GA	T	CA	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	720
Db	71419	CG	CA	GT	GA	T	CA	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	71478
QY	721	GG	GG	CG	CA	TC	CG	GG	CT	CA	AG	GT	CT	CG	CG	AT	CA	AT	AG	CG	CG	780
Db	71479	GG	GG	CG	CA	TC	CG	GG	CT	CA	AG	GT	CT	CG	CG	AT	CA	AT	AG	CG	CG	71538
QY	781	CG	CT	AT	GG	CT	GA	C	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	840
Db	71539	CG	CT	AT	GG	CT	GA	C	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	71598
QY	841	TG	GG	GG	CA	CT	T	CG	AT	G	T	CT	C	CA	AT	T	G	AG	CG	CG	CG	900
Db	71599	TG	GG	GG	CA	CT	T	CG	AT	G	T	CT	C	CA	AT	T	G	AG	CG	CG	CG	71658
QY	901	CA	CT	G	CG	AG	TA	CC	CA	CT	T	G	AG	AG	AG	AG	AG	AG	AG	AG	AG	960
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QY	961	CA	TG	GA	GA	AT	CC	CG	CG	AG	CA	CT	G	AG	AG	AG	AG	AG	AG	AG	AG	1020
Db	71719	CA	TG	GA	GA	AT	CC	CG	CG	AG	CA	CT	G	AG	AG	AG	AG	AG	AG	AG	AG	71778
QY	1021	CAG	GT	CG	CA	CAG	CT	GT	G	AG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	1080
Db	71779	CAG	GT	CG	CA	CAG	CT	GT	G	AG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	71838
QY	1081	CT	G	AG	AG	TA	GA	CT	CT	G	T	CG	GG	CG	T	G	AG	CT	CT	CA	AG	1140
Db	71839	CT	G	AG	AG	TA	GA	CT	CT	G	T	CG	GG	CG	T	G	AG	CT	CT	CA	AG	71898
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Qy 2401 CTTTCACCTATATTTTGTGTAATTTTGTACTGTATGATGAATTTTGTATGTAATAA 2460
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LOCUS CQ730982 1914 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16916 from Patent WO02068579.
ACCESSION CQ730982
VERSION CQ730982.1 GI:42306299
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 16916 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 1914
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 36.6%; Score 913; DB 2; Length 1914;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Qy 233 ATGCAGGCCCCCAGCGGAGCTCGCGTGGGCATCGACCTGGGCACCACTACTCTGTCGCTG 292
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Qy 353 CCCAGCTACGCGGCTTACCGACACCGAGCGGCTGTCGGGACGCGGCACAGAGCCAG 412
Db 121 CCCAGCTACGCGGCTTACCGACACCGAGCGGCTGTCGGGACGCGGCACAGAGCCAG 180
Qy 413 GCGGCCCTGAACCCCAACACCGCTGTTGATGCCAAGGGCTGATCGGGCGCAAGTTC 472
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Qy 473 GCGGACACCGGTCAGTGCGGACATGAAGCATCTGGGCTTTCAGGTGGTGAGGAGGGC 532
Db 241 GCGGACACCGGTCAGTGCGGACATGAAGCATCTGGGCTTTCAGGTGGTGAGGAGGGC 300
Qy 533 GCGAAGCCCAAGGTCGCGTATGCTACCGGGGGAGGACAGAGCTTACCCCGAGGAG 592
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RESULT 5

BC035665

LOCUS

DEFINITION

Homo sapiens

heat shock

2279 bp

mRNA

linear

PRI 09-DEC-2005

HSP70B', mRNA (cDNA clone

ACCESSION	MGC:46216 IMAGE:5723718), complete cds.	gene	/note="Vector: pCMV-SPORT6"
VERSION	BC035665.1 GI:23274231		1..2279
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SOURCE	Homo sapiens (human)		/db_xref="GeneID:3310"
ORGANISM	Homo sapiens		/db_xref="HGNC:5239"
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		/db_xref="IMGT/GENE-DB:5239"
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		110..2041
	Hominidae; Homo.		/gene="HSPA6"
REFERENCE	1 (bases 1 to 2279)	CDS	/codon_start=1
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Tothiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Male, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Mullan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		/translation="MQAPRELAVGIDLTGTYSCVGFQQRVEILLANDQNRTPSVV AFTDRLVDAKQAALNPHNFDKALIGRKFPADTTVQSDMGHWFRVYVEGSK PKRVVCYRGEDKTFYEEISSMVLSSMKETAAYLGPVKHAVITVPFNDSDQAT KDAGATAGNLVRIINEPTAAATAYGLDRRGAGERNVLI FDLGGGTDFVSLSDAGV PEVKATAGTHLGGEDFDNRLNVNFMEEFRKHGKDLGNGKRALRLTACERAKRTL SSQTATLEIDSLFEGVDFTYSTRARFELNSINDEAVAGAAVOALMDKCKVQD DVVLVGSTRIKPKVQLQDFNGLKNSINPEDEAVAGAAVOALMDKCKVQD LLLDVAPLSLGLTAGGVMVTLIQRNATLPTKQTQTFITYSDNQGVFIQVYEGRA MKNONLLGRFELSGIPAPRGVPOIEVTFDIDANGILSVTATDRSKKAKLITIND KGRLSKEEVRVMYHEAOYKABEQADQRAKNSLEAHVHVYKGLSLESLDKKPIE EDRRKMDKREVLNLEHNLAEKEEYEHQKELEQICRPISRLYGGFVPGGSSC GTQARQDPSTGPIIEVD"
CONSTRM	Mammalian Gene Collection Program Team		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2279)		
AUTHORS	NIH MGC Project		
CONSTRM	Direct Submission		
TITLE	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA		
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov		
REMARK	Contact: MGC help desk		
COMMENT	Email: cgapbs@mail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland. Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@hri.nih.gov Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McLoakey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Teague, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov		
source	Series: IRAC Plate: 79 Row: 9 Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 42822885. Location/Qualifiers		
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	/lab_host="DH10B"		
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	QY 194 GCCTCGTGGGCTCCAGCATCCGACAAGAGCTTTCAGCATGCGAGGCCCAACGGAGGCTC 253		
	Db 71 GCCTCGTGGGCTCCAGCATCCGACAAGAGCTTTCAGCATGCGAGGCCCAACGGAGGCTC 130		
	QY 254 GCGTGGGCGATCGACCTGGGCAACCACTACTCTGCTGGGGGGCTGTTTCAGCAGGGCGCG 313		
	Db 131 GCGTGGGCGATCGACCTGGGCAACCACTACTCTGCTGGGGGGCTGTTTCAGCAGGGCGCG 190		
	QY 314 GTGGAGATCTTGGGCCAACGACAGGGGCAACCGGCGAACCGGCGAACCGGCGCTTCCACC 373		
	Db 191 GTGGAGATCTTGGGCCAACGACAGGGGCAACCGGCGAACCGGCGAACCGGCGCTTCCACC 250		
	QY 374 GACACCGAGCGGCTGGTCCGGGAGACCGGCGCAAGAGCCAGGGCGGCCCTGNAACCCCAAC 433		
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	QY 554 TGTACCGCGGGAGGACAAAGACGTTCTACCCCGAGGAGATCTCGTCCATGTTGCTGAGC 613		
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RESULT 6
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LOCUS Homo sapiens mRNA for heat shock 70kDa protein 6 (HSP70B') variant,
DEFINITION clone: FCC101B10.
ACCESSION AK223362
VERSION AK223362.1 GI:62898284
KEYWORDS FLI_CDNA; oligo capping.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1

AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
REFERENCE
TITLE
JOURNAL
PUBMED
AUTHORS
COMMENT
FEATURES
source
CDS
ORIGIN

Maruyama,K. and Sugano,S.
Oligo-capping: a simple method to replace the cap structure of
eukaryotic mRNAs with oligoribonucleotides
Gene 138 (1-2), 171-174 (1994)
8125298
2
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S.
Construction and characterization of a full length-enriched and a
5'-end-enriched cDNA library
Gene 200 (1-2), 149-156 (1997)
9373149
3 (bases 1 to 2318)
Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A. and
Yokoyama,S.
Direct Submission
Submitted (22-APR-2005) Akiko Tanaka, RIKEN Yokohama Institute,
Protein Research Group; 1-7-22 Suehiro, Tsurumi, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:aktanaka@riken.jp,
URL: http://protein.gsc.riken.jp/, Tel:81-45-503-9452,
Fax:81-45-503-9450)
This work was supported in part by the National Project on Protein
Structural and Functional Analysis, Ministry of Education, Culture,
Sports, Science and Technology of Japan.
Location/Qualifiers
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Qy 134 GCAGAGAAACCGCAGGAGAGGCTCACTGCTGAGCGCCCTCGACCGCGGAGCGGAGCA 193
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Qy 314 GTGGAGATCCTGGCCAAACGACGAGGGGCAACCGCACCGCCAGCTACGTGGCTTCAACC 373

```

Contact: vegas@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
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2677..2745
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Db													
RESULT 7	AL590385												
LOCUS	Human DNA sequence from clone RP11-5K23 on chromosome 1 Contains												
DEFINITION	the FCGR2A gene for Fc fragment of IgG low affinity IIA receptor												
	for (CD32), the HSPA6 gene for heat shock 70kDa protein 6												
	(HSP70B), a ribosomal protein S23 (RPS23) pseudogene, the FCGR3A												
	gene for Fc fragment of IgG low affinity IIA receptor for (CD16),												
	a novel gene and three CpG islands, complete sequence.												
ACCESSION	AL590385 AC013307												
VERSION	AL590385.23 GI:48374143												
KEYWORDS	HTG; FCGR2A; FCGR3A; HSPA6; RPS23.												
SOURCE	Homo sapiens (human)												
ORGANISM	Homo sapiens												
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;												
	Hominidae; Homo.												
	1 (bases 1 to 129505)												
REFERENCE	Lovell, J.												
AUTHORS	Direct Submission												
TITLE	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,												
JOURNAL	Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk												
	Clone requests: clonerequest@sanger.ac.uk												
	On Jun 6, 2004 this sequence version replaced gi:21211764.												
	Draft Sequence Produced by Whitehead Institute/MIT Center for												
	Genome Research, 320 Charles Street,												
	Cambridge, MA 02141, USA												
	http://www-seq.wi.mit.edu												
	The following abbreviations are used to associate primary accession												
	numbers given in the feature table with their source databases:												
	Emi, EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information												
	on the WORMPEP database can be found at												
	http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence												
	was generated from part of bacterial clone contigs of human												
	chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping												
	Group. Further information can be found at												
	http://www.sanger.ac.uk/HGP/Chr1												
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	Pieter de Jong. For further details see												

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Query Match      19.9%; Score 495; DB 5; Length 129505;
Best Local Similarity 99.8%; Pred. No. 7.3e-286;
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VERSION AR531647.1 GI:53920086
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2336)
AUTHORS Kaser, M.R.
TITLE Genes expressed in treated human C3A liver cell cultures
JOURNAL Patent: US 6727066-A 203 27-APR-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
Location/Qualifiers

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ACCESIO		
VERSION		
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ORGANI		

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QY	632	GAGGCGTACCTGGGCGAGCGCGTGAAGCAACGAGTATCACCGTGGCCCACTATTTCAGT	691			
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QY	692	AACCTCGCAGCGCCAGGCCCAACAAAGACGCGGGGGCCATCGCGGGCTCAAGTGTGCGG	751			
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AK093925
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AK093925
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AK093925 2253 bp mRNA linear PRI 20-JAN-2006
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AK093925.1 GI:21752885
oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1

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14702039

2

Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Moniyan, H., Onogawa, S., Kasriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Kataoka, K., Kuga, N., Kuroda, A., Satoh, I., Kanata, K., Takami, S., Teraohima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project Unpublished

3 (bases 1 to 2253)

Isogai, T. and Yamamoto, J. Direct Submission

Submitted (04-JUL-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: flj-cdna@ifty.com, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

1. .2253

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TRACH2015654"

/tissue_type="trachea"

/clone_lib="TRACH2"

/notes="cloning vector: pME18SFL3"

ORIGIN

Query Match 17.8%; Score 444; DB 5; Length 2253;

Best Local Similarity 99.6%; Pred. No. 5e-255;

Matches 544; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 134 GCAGAGAAACCGCAGGAGAGCTCACTGCTGAGCGCCCTCGACGGCGGAGCGGAGCA 193

DB 21 GCAGAGAAACCGCAGGAGAGCTCACTGCTGAGCGCCCTCGACGGCGGAGCGGAGCA 80

QY 194 GCCTCGTGGCTTCCAGCATCCGACAGAGCTTCAGCCATGACGAGCCGCCACGGAGCTC 253

DB 81 GCCTCGTGGCTTCCAGCATCCGACAGAGCTTCAGCCATGACGAGCCGCCACGGAGCTC 140

QY 254 CGCGTGGGATCGACCTGGGACACACTACTCTGCTGGGCGCTGTTTACGAGGCGCGC 313

DB 141 CGCGTGGGATCGACCTGGGACACACTACTCTGCTGGGCGCTGTTTACGAGGCGCGC 200

QY 314 GTGAGATCTGCGCAACGACGAGGCAACCGCACCGCCAGCGCTACGTGGCTTCACC 373

DB 201 GTGAGATCTGCGCAACGACGAGGCAACCGCACCGCCAGCTACGTGGCTTCACC 260

QY 374 GACACGAGCGGTGTGTCGGGAGCGCGGCCAAGAGCGAGCGCGCTTGAACCCCAACAC 433

DB 261 GACACGAGCGGTGTGTCGGGAGCGCGGCCAAGAGCGAGCGCGCTTGAACCCCAACAC 320

QY 434 ACCGTGTTGATGCCAAGCGGCTGATCGGCGCGCAAGTTTCGCGACACCAACGTCAGTCG 493

Db 321 ACCGTGTTGATGCCAAGCGGCTGATCGGCGCGCAAGTTCGCGGACACACCGTGCAGTCG 380

QY 494 GACATGAAGCACTGGCCCTTCAGGTGTGAGCGGCGGCGGCAAGCCCAAGGTGCGGCTA 553

Db 381 GACATGAAGCACTGGCCCTTCAGGTGTGAGCGGCGGCGGCAAGCCCAAGGTGCGGCTA 440

QY 554 TGCTACCGCGGGAGGACAAAGACGTTTACCCCGGAGGAGATCTCGTCCATGGTGTGAGC 613

Db 441 TGCTACCGCGGGAGGACAAAGACGTTTACCCCGGAGGAGATCTCGTCCATGGTGTGAGC 500

QY 614 AGATGAAGGAGACGCGCGGCGGTACTCTGGGCGGAGCCCGTGAAGCAGCGAGTCATCACC 673

Db 501 AAAGTGAAGGAGACGCGCGGCGGTACTCTGGGCGGAGCCCGTGAAGCAGCGAGTCATCACC 560

QY 674 GTGCC 679

Db 561 GTGCC 566

RESULT 10

LOCUS BX537284 136035 bp DNA linear HTG 20-JUN-2003

DEFINITION Homo sapiens chromosome 1 clone XX-86542C10, 2 unordered pieces.

ACCESSION BX537284

VERSION BX537284.3 GI:32134910

KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 136035)

GLITCHERO, R. Direct Submission

Submitted (19-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

On Jun 20, 2003 this sequence version replaced gi:31620806.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: fwp6542C10

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 32214 bases at least Q40

Consensus quality: 32390 bases at least Q30

Consensus quality: 36787 bases at least Q20

Insert size: 135335; sum-of-contigs

Insert size: 38793; 21.5% error; agarose-fp

Quality coverage: 10.50x in Q20 bases; sum-of-contigs Quality coverage: 38.74x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 107755: contig of 107755 bp in length

* 107756 107755: gap of 100 bp

* 107856 136035: contig of 28180 bp in length.

Location/Qualifiers

1. .136035

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="1"

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misc_feature 1..107755
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 4.6e-255;
Matches 544; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 134 GCAGAGAAACCGCAGGAGAGCCTCACTGCTGAGCGCCCTCGACGGCGGAGCGGAGCA 193
Db 106478 GCAGAGAAACCGCAGGAGAGCCTCACTGCTGAGCGCCCTCGACGGCGGAGCGGAGCA 106537

Qy 194 GCCTCCGTGGCCTCCAGCATCCGACAGAAAGCTTCAAGCCATGAGCGCCCAAGGAGCTC 253
Db 106538 GCCTCCGTGGCCTCCAGCATCCGACAGAAAGCTTCAAGCCATGAGCGCCCAAGGAGCTC 106597

Qy 254 GCGGTGGGATCGACCTGGGACACCACTACTCGTGTGGGCGTGTTCAGCAGGCGCGC 313
Db 106598 GCGGTGGGATCGACCTGGGACACCACTACTCGTGTGGGCGTGTTCAGCAGGCGCGC 106657

Qy 314 GTGAGATCTCTGGCCACGACAGGCAACCGCACCGCCAGCTACGTGGCCTTCACC 373
Db 106658 GTGAGATCTCTGGCCACGACAGGCAACCGCACCGCCAGCTACGTGGCCTTCACC 106717

Qy 374 GACACCGAGCGGCTGTGTCGGGACCGCGCCAGAGCAGCGCGGCGCTGAACCCCAAC 433
Db 106718 GACACCGAGCGGCTGTGTCGGGACCGCGCCAGAGCAGCGGCGGCTGTGAACCCCAAC 106777

Qy 434 ACCGTGTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACCAAGTCGATCG 493
Db 106778 ACCGTGTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACCAAGTCGATCG 106837

Qy 494 GACATGAAGCACTGGCCCTTCAGGTGTGAGCGAGCGGCGGCAAGCCCAAGTCGGGTA 553
Db 106838 GACATGAAGCACTGGCCCTTCAGGTGTGAGCGAGCGGCGGCAAGCCCAAGTCGGGTA 106897

Qy 554 TGTACCGCGGGAGAGACAGTCTTACCCCGAGGAGATCTCTCCATCGTGTGTGAGC 613
Db 106898 TGTACCGCGGGAGAGACAGTCTTACCCCGAGGAGATCTCTCCATCGTGTGTGAGC 106957

Qy 614 AAGATGAAGGAGACGCGCGGAGCGTACCTGGGCGAGCGGCGGTAAGCAGCAGTATCACC 673
Db 106958 AAGATGAAGGAGACGCGCGGAGCGTACCTGGGCGAGCGGCGGTAAGCAGCAGTATCACC 107017

Qy 674 GTGCC 679
Db 107018 GTGCC 107023

RESULT 11
AR454599 AR454599 2962 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 72 from patent US 6682888.
DEFINITION AR454599
ACCESSION AR454599
VERSION AR454599.1 GI:42688068
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2962)
TITLE Loring,J.F., Tingley,D.W. and Edwards,C.M.
JOURNAL Genes expressed in alzheimer's disease
Patent: US 6682888-A 72 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
source 1..2962
/mol_type="genomic DNA"

ORIGIN
Query Match 17.3%; Score 431; DB 2; Length 2962;
Best Local Similarity 99.8%; Pred. No. 3.6e-247; Indels 0; Gaps 0;
Matches 481; Conservative 0; Mismatches 1;

Qy 198 CCGTGGCTCCAGCATCCGACAGAAAGCTTCAAGCCATGAGCGCCCAAGGAGCTCGCG 257
Db 699 CCGTGGCTCCAGCATCCGACAGAAAGCTTCAAGCCATGAGCGCCCAAGGAGCTCGCG 758

Qy 258 TGGGCATCGACCTGGGACCAACCTACTCGTGTGGGCGTGTTCAGCAGGCGCGTGG 317
Db 759 TGGGCATCGACCTGGGACCAACCTACTCGTGTGGGCGTGTTCAGCAGGCGCGTGG 818

Qy 318 AGATCTGGCCAGCAGCGGCAACCGCACCGCCAGCTACGTGGCCTTCACCGACA 377
Db 819 AGATCTGGCCAGCAGCGGCAACCGCACCGCCAGCTACGTGGCCTTCACCGACA 878

Qy 378 CCGAGCGGCTGTGTCGGGACCGCGCCAAAGAGCGGCGGCGCTGAAACCCCAACACCG 437
Db 879 CCGAGCGGCTGTGTCGGGACCGCGCCAAAGAGCGGCGGCGCTGAAACCCCAACACCG 938

Qy 438 TGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACACCGTGCAGTCGACA 497
Db 939 TGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTTCGGGACACACCGTGCAGTCGACA 998

Qy 498 TGAAGCACTGGCCCTTCAGAGTGTGAGCGGCGGCAAGCCCAAGTGGCGGTATGCT 557
Db 999 TGAAGCACTGGCCCTTCAGAGTGTGAGCGGCGGCAAGCCCAAGTGGCGGTATGCT 1058

Qy 558 ACCGCGGGAGAGCAAGAGCTTACCCCGAGGAGATCTCGTCCATGTGTGAGCAAGA 617
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Qy 618 TGAAGAGACGCGCGGAGCGTACCTGGGCGAGCCCGTGAAGCAGCAGTATCAGCTGC 677
Db 1119 TGAAGAGACGCGCGGAGCGTACCTGGGCGAGCCCGTGAAGCAGCAGTATCAGCTGC 1178

Qy 678 CC 679
Db 1179 CC 1180

RESULT 12
BV198650 401 bp DNA linear STS 10-JUN-2004
LOCUS sgml198410 Human DNA (sequenom) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV198650
VERSION BV198650.1 GI:48166754
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Homnidae; Homo.
COMMENT 1 (bases 1 to 401)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.N. and Braun,A. Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 401
Location/Qualifiers
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source 1. .401
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STS
ORIGIN

Query Match 14.0%; Score 350; DB 7; Length 401;
Best Local Similarity 99.8%; Pred. No. 3.1e-198;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1903 GCCTTAGGACAAAGTCCGAGAGACAGGCGCAAGTGCAGGAAG 1962
Db 1 GCCTTAGGACAAAGTCCGAGAGACAGGCGCAAGTGCAGGAAG 60

Qy 1963 TCCTTGCTGGCTGGAGACAAACAGCTGGCAGAGAGAGGAGTATGACATCAGAGA 2022
Db 61 TCCTTGCTGGCTGGAGACAAACAGCTGGCAGAGAGAGGAGTATGACATCAGAGA 120

Qy 2023 GGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCAGGCTCTATGGGGGGCTTGGTGTC 2082
Db 121 GGGAGCTGGAGCAAAATCTGTGCGCCCATCTTCTCAGGCTCTATGGGGGGCTTGGTGTC 180

Qy 2083 CTGGGGGAGAGTTGTAGGCTCAAGCCCAAGGGGGACCCAGACACCGGGCCCATCA 2142
Db 181 CTGGGGGAGAGTTGTAGGCTCAAGCCCAAGGGGGACCCAGACACCGGGCCCATCA 240

Qy 2143 TTGAGGAGTTGATGTAATGGCCCTTCGTATAGTACGTGACGTGACGTGATGCTATGC 2202
Db 241 TTGAGGAGTTGATGTAATGGCCCTTCGTATAGTACGTGACGTGACGTGATGCTATGC 300

Qy 2203 TATGGGCTCTAGACTGTCTTATGATCTGCGCTTCAAGATGAAGGGCTTGGGGG 2262
Db 301 TATGGGCTCTAGACTGTCTTATGATCTGCGCTTCAAGATGAAGGGCTTGGGGG 360

Qy 2263 GTCTTCCCTCAAAGCTAGAACTTTCTTCCAGATAACTG 2303
Db 361 GTCTTCCCTCAAAGCTAGAACTTTCTTCCAGATAACTG 401

RESULT 13
S78631
LOCUS 1001 bp DNA linear PRI 07-MAY-1993
DEFINITION HSPA6=70-kda heat-shock protein [human, Genomic, 1001 nt].
ACCESSION S78631
VERSION S78631.1 GI:244243
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1001)
Leung,T.K., Hall,C., Rajendran,M., Spurr,N.K. and Lim,L.
The human heat-shock genes HSPA6 and HSPA7 are both expressed and
localize to chromosome 1
Genomics 12 (1), 74-79 (1992)
1346391
PUBMED
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gisseq 78631] from the original journal article.
FEATURES
source
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e-185;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGAGCTCCGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATCGAGCCCCACG 246
Db 205 GGCAGAGCTCCGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATCGAGCCCCACG 264

Qy 247 GGAGCTCGCGTGGGATCGACCTGGGACCACTACTCTGCTGGGGGTGTTTCAGCA 306
Db 265 GGAGCTCGCGTGGGATCGACCTGGGACCACTACTCTGCTGGGGGTGTTTCAGCA 324

Qy 307 GGGCCCGTGGAGATCTCTGGCCAAACAGCAGGGCAACCGCACCGCCAGCTACGTGC 366
Db 325 GGGCCCGTGGAGATCTCTGGCCAAACAGCAGGGCAACCGCACCGCCAGCTACGTGC 384

Qy 367 CTTTACCGACACCGAGCGCTGTGGGGACCGGCAAGAGCCAGCGCGCCCTGAACCC 426
Db 385 CTTTACCGACACCGAGCGCTGTGGGGACCGGCAAGAGCCAGCGCGCCCTGAACCC 444

Qy 427 CCACAAACACGTGTTTCGATGCCAAGCGGTGATCGGGCGCAAGTTTCGCGACACCA 486
Db 445 CCACAAACACGTGTTTCGATGCCAAGCGGTGATCGGGCGCAAGTTTCGCGACACCA 504

Qy 487 GCAGTCGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGACATGAAGCACTGGCCCTTCC 533

RESULT 14
AX336488 2492 bp DNA linear PAT 09-JAN-2002
Sequence 6997 from Patent WO0194629.
ACCESSION AX336488
VERSION AX336488.1 GI:18127207
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1
Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
gene sets
Patent: WO 0194629-A 6997 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source
1. .2492
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 13.2%; Score 329; DB 2; Length 2492;
Best Local Similarity 100.0%; Pred. No. 1.4e-185;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 GGCAGAGCTCCGTGGCTCCAGCATCCGACAAGAGCTTCAGCCATCGAGCCCCACG 246
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Qy 247 GGAGCTCGCGTGGGATCGACCTGGGACCACTACTCTGCTGGGGGTGTTTCAGCA 306
Db 265 GGAGCTCGCGTGGGATCGACCTGGGACCACTACTCTGCTGGGGGTGTTTCAGCA 324

Qy 307 GGGCCCGTGGAGATCTCTGGCCAAACAGCAGGGCAACCGCACCGCCAGCTACGTGC 366
Db 325 GGGCCCGTGGAGATCTCTGGCCAAACAGCAGGGCAACCGCACCGCCAGCTACGTGC 384

Qy 367 CTTTACCGACACCGAGCGCTGTGGGGACCGGCAAGAGCCAGCGCGCCCTGAACCC 426
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Qy 427 CCACACACCGTGTTCGATCCCAAGCGGCTGATCGGGCGCAAGTTCGCGGACACCAACGGT 486
Db 445 CCACACACCGTGTTCGATCCCAAGCGGCTGATCGGGCGCAAGTTCGCGGACACCAACGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

RESULT 15
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LOCUS Human heat-shock protein HSP70B, gene.
DEFINITION X51757
ACCESSION X51757
VERSION X51757.1 GI:35221
KEYWORDS heat shock protein; heat shock protein 70; heat shock protein
HSP70B; hsp70B gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo
1 (bases 1 to 2492)
Leung,T.K., Rajendran,M.Y., Monfries,C., Hall,C. and Lim,L.
The human heat-shock protein family. Expression of a novel
heat-inducible HSP70 (HSP70B) and isolation of its cDNA and
genomic DNA
Biochem. J. 267 (1), 125-132 (1990)
2327978
2 (bases 1 to 2492)
Rensing,S.A. and Maller,U.G.
Phylogenetic analysis of the stress-70 protein family
J. Mol. Evol. 39 (1), 80-86 (1994)
7545947
3 (bases 1 to 2492)
Hall,C.
Direct Submission
Submitted (01-FEB-1990) Hall C., Institute of Neurology, Dept of
Neurochemistry, 1 Wakefield Street, London WC1N 1PU, UK
See <X51758> for partial HSP70B' cDNA.

FEATURES
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/db_xref="taxon:9606"
/cell_line="SHA"
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102..106
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251..2182
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/db_xref="GOA:P17066"
/db_xref="UniProtKB/Swiss-Prot:P17066"
/translations="MQAPRELAVGIDLTFTYSCVGFQQGRVEILLANDQGNRTTSPYV
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polyA_signal
2363..2368
polyA_signal
2467..2472
ORIGIN

Query Match 13.2%; Score 329; DB 5; Length 2492;
Best Local Similarity 100.0%; Pred. No. 1.4e-185; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 187 GGACGACGCTCCGTTGGCTCCAGCATCCGACCAAGAGCTTCAGCCATGCGGCCCCACG 246
Db 205 GGACGACGCTCCGTTGGCTCCAGCATCCGACCAAGAGCTTCAGCCATGCGGCCCCACG 264
Qy 247 GGAGCTCGCGTGGGCGATCGACCTGGGCAACCACTTACTCGTGGCGGTGTTTCAGCA 306
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Qy 307 GGGCGCGTGGAGATCTCTGGCCAAACAGCGGCAACCGCACCCAGTACGTGGC 366
Db 325 GGGCGCGTGGAGATCTCTGGCCAAACAGCGGCAACCGCACCCAGTACGTGGC 384
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Db 385 CTTACCCGACACCGAGCGGCTGGTGGGGAACCGGCCAAGAGCCAGGCGGCTGAACCC 444
Qy 427 CCACACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCGCGGACACCAACGGT 486
Db 445 CCACACACCGTGTTCGATGCCAAGCGGCTGATCGGGCGCAAGTTCGCGGACACCAACGGT 504
Qy 487 GCAGTCGGACATGAAGCACTGGCCCTTCC 515
Db 505 GCAGTCGGACATGAAGCACTGGCCCTTCC 533

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Job time: 13829.4 secs